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BG551208 sad334e05.
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## BG551127 491 bp sad33f01.y1 Gm-c1074 ID: Gm-c1074-2162 5' ## BG551127 BG551127.1 GI:13562907 BG557. mRNA sequence. mRNA EST 09-APR-2001 Glycine max cDNA clone GENOME SYSTEMS CLONE similar to TR:Q9SVI4 Q9SVI4 ES43 LIKE PROTEIN

soybean

Glýcine max gradiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Phaseoleae; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurt, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurt, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Beck, C.,

EST Project

Unpublished (1999)
Contact: Sheemaker R/Public Soybean EST F
public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. L
Tel: 314 286 1800
Fax: 314 286 1810 St. Louis, MO 63108, USA

Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
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                                                                                                                                                                                                                                                                                        Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                      Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project
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(hypersensitive response) by vacuum infiltrating plant
tissue with Pseudomonas syringae pv. glycinea carrying the
avrB gene (Genetics 14:1597-1604). Plant tissue (expanded
unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36,
and 53 hrs after inoculation and their mRNA pooled equally
for cDNA construction. The library was prepared using the
Stratagene pBluescript II SK(+) library construction kit.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with an XhoI restriction
site. EcoRI adaptors were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The CDNA insert is
protected from XhoI digestion via methylation during first
strand synthesis. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into E.coli ElectroMax DHIOB host cells. Plant
care, inoculations, and library construction were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  performed by Steve Clough (Lila Vodkin lab, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
xhoI; The cDNA library was constructed from mRNA isolated
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/lab_host="DH10B"
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response)"
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/clone_lib="Gm-c1074"
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                AW761136 530 bp mRNA EST 21-NOV-2000 s163f12.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-6024 5' similar to TR:065462 065462 RECEPTOR LIKE PROTEIN
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Rosidae; eurosids I; Fabales; Fabaceae;
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-/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      care, inoculations, and library construction were performed by Steve Clough (Lila Vodkin lab, University of Illinois)."

140 c 129 g 109 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: xhoI; The cDNA library was constructed from mRNA isolated from 9-11 day old seedlings that were induced for HR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="GENOME SYSTEMS CLONE ID: Gm-c1074-2145"
/clone_lib="Gm-c1074"
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100.0%; Pr
     Keim, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44;
Pred. No.
  Vodkin,L.,
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                                                                                                         Streptophyta; Embryophyta; Tracheophyta; yta; eudicotyledons; core eudicots;
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  Erpelding, J., Coryell, V., Khanna
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                                                                                   Papilionoideae;
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407 GTATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com.or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 420.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             info@genomesystems.com web site: www.genomesystems.com
Insert Length: 1680 Std Error: 0.00
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                                                                                                  Similarity
                                                                                                                                                                                                         136
                                                                                                                                                                                                             e,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Materston,R. and Wilson,R.
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal of mRNA was used for CDNA synthesis. Stratagene's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthexix Kit (catalog number 200401) was used to synthesize the cDNA. First- stranded synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XhoI; This cDNA library was constructed from mRNA isolated from cotyledons of 3- and 7-day-old Williams seedlings which were propagated on paper towels with distilled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="cotyledons of 3- and 7-day-old Williams
seedlings"
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1027-6024"
/clone_lib="Gm-c1027"
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1.8e-13;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 437-3222 FAX: [888]919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome
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(217) 333-4582
                                                                                                                                                                                                                             /note="vector: pBluescript II xR; Site_1: EcoRI; Site_2: xhoI; Library Gm-r1021 is a sequence-driven, reracked set of the original library Gm-c1004 which was prepared from root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. The Gm-c1004 library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, Az 86011, email: paul.keim@enu.edu, virginia.coryell@nau.edu. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Computational Biology Centers, University of Minnesota.
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                                                                                     Center for Comparative and Functional University of Illinois,
                            http://www.life.uiuc.edu/biotech/keck.html."
161 c 151 g 193 t 20 others
                                                                                                                                                 http://www.genomesystems.com,
                                                                                                                                                                                                          http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
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/lab_host="XL10-Gold"
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                                                                                                                                              Reracking was performed by Genome Systems, St. Louis, ttp://www.genomesystems.com, and sequencing by the Keck
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert Length: 1008 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 6332 For further information call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shoemaker R/Public Soybean EST Project
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Ritter, E., Kohn, S., Shin, T
Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 380.
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314 286 1810
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       Conservative
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                                                                                                                                                      Erpelding.
                                                                                                                                                                                                                          cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLIO-Gold host cells. This library
                                                                                                                                                                                                                                                                                                    XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally
                                                                                                                                                                                                     constructed by Dr. Randy Shoemaker and Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                     XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Mature flowers, field grown plants"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="GENOME SYSTEMS CLONE ID: Gm-c1015-5652"
/clone_lib="Gm-c1015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Glycine max"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
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                                                  Length 540;
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  Gaps
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Vodkin, L.O., PI, A Functional Genomics Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_ESTs: AW432561 corresponding to Gm-c1015-5652 (5')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae,
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GM700009B10H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ystems.com web site:www.genomesystems.com
Seq primer: 5'.TTTTTTTTTTTTTTTTTTT(A/C/G)-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427-3324 or contact:clones@genomesystems.com or info@genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
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(217) 333-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. A., Director,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-vodkin@uiuc.edu
  þ
                                                                                                                                                                                                                                                                                                                                                                                                     various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-ri070. The cDNA clones of the reracked Gm-ri070 library were then sequenced at the 3' end. The
                                                                    information on the source library for each clone can be obtained by referring to the Genome Systems clone
                                                                                                                      http://www.life.uiuc.edu/biotech/keck.html.corresponding 5' EST from each clone in the library is listed in the 'OTHER EST' field.
                                                                                                                                                                                                                          Reracking was performed by Genome Systems, St. Louis, http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics,
                                                                                                                                                                                                                                                                                                                              contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota,
                                                                                                                                                                                                        University of Illinois,
                                                                                                                                                                                                                                                                                                      http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     set of 9,216 clones selected from cDNA libraries from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Gm-r1070"
/note="The library Gm-r1070 is a sequence-driven,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3847"
/clone="Gm-r1070-3447"
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                               original cDNA library that is also listed under
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Genome Systems clone ID of
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The detailed Note:

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VERSION ACCESSION

AW586761 514 bp mRNA EST 07-SEP-20 EST318384 MHAM Medicago truncatula/Glomus versiforme mixed library cDNA clone pMHAM-55G12, mRNA sequence.

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 349
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: jwallace@u.washington.edu
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
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HS_5183_Al_B08_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=759 Col=15 Row=C, DNA sequence.
                                            Similarity 100
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.htsc.washington.edu
Plate: 759 row: C column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 Queen Anne Avenue North, Seattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC,
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ451805.1 GI:4592975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 349)
                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (206) 616-3618
(206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                               /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially disested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

a 79 c 86 g 101 t
                                                                                                                                                                                                                                                                                          /clone="Plate=759 Col=15 Row=C"
/clone_lib="RPCI-11 Human Male
                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                            100.0%;
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                                                                                  17.18;
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                                                          Score 21; DB 13; Length 349; Pred. No. 0.53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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0.0011;
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                                                                                                                                                                                                                                                                                          Male BAC Library"
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                                                      RESULT
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BE999004
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Best Local
            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle,
Tel: 612 625 5715
Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://chrysie.tamu.edu/medicago
Seg primer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M272982e TIGR sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fedorova,M., Pierson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P., Town,C.D., Bowman,C.L., Craven,M.B., Cho,J. and Fraser,C.M. ESTs from senescent nodules of Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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BE999004
                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE999004 457 bp mRNA EST 06-OCT-20 EST430727 GVSN Medicago truncatula cDNA clone pGVSN-13D16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula
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                                                                                                                                                     126
          Conservative
                                                                                                                                      // note="Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2: XhOI; cDNA was prepared from polyA+ enriched RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="senescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old
plants harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="pGVSN-13D16"
/clone_lib="GVSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Medicago truncatula"
/cultivar="genotype_A17"
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                              17.1%;
100.0%;
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                           Score 21; DB 11;
Pred. No. 0.54;
     Mismatches
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Gaps
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KEYWORDS

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RESULT 1
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Best Local Similarity
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The Samuel Roberts Noble Foundation
OK 73401, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medicago truncatula/Glomus versiforme mixed EST library. Medicago truncatula/Glomus versiforme mixed EST library Eukaryota; mixed EST libraries.
                                                                                                                                                                                                                BF650924
BF650924.1
                                                                                                                                                                                                                                                        BF650924 539 bp mRNA EST 20-DEC-2000 NF098E01EC1F1005 Elicited cell culture Medicago truncatula cDNA clone NF098E01EC 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'http://chrysie.tamu.edu/medicago'
Seq primer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
                                                                 Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2510 Sam Noble Parkway, Ardmore, Tel: 580-223-5810 Fax: 580-221-7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Maria J. Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
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Torres-Jerez,I.,
                                                                                                                                                                                            EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR sequence name:MTDAV42TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Noble EST name: N255126e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mjharrison@noble.org
                                                                                                                                                                   barrel medic
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                      (bases 1 to 539)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
/dev_stage="Roots harvested at 10, 122, 31 and 38 days
/dev_stage="Roots harvested at 10, 122, 31 and 38 days
/post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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/clone="рмнам-55G12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib-"MHAM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cultivar="Medicago truncatula genotype A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Medicago truncatula/Glomus versiforme mixed EST
                                                                                                                                                                                                                   GI:11916054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.1%;
Scott, A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No.
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Harris, A.R.,
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0.54;
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Gonzales, R.A.,
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Bell,C.J.
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AUTHORS
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Best Local
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BE124753
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Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                       Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle
Tel: 612 625 5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 539 Std Error: 0.0
Plate: 098 row: E column: 01
Seq primer: TCACACAGGAAACAGCTATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Dixon RA
                                                                                                                                                                                                                                       ,n., Ellis,L., Town,C.D., Bowman,C.L., Holt,I.E. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST393788 GVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
                                                 Fax: 651-649-5058
Email: vance004@maroon.tc.umn.edu
University of Minnesota name:M261021e
                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                        barrel medic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE124753.1
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                               TIGR sequence name:MTCCC28TK
                                                                                                                                                                                                                           truncatula
                                                                                                                                                                                                                                             ESTs from one month old nitrogen-fixing root nodules of Medicago
More information is available at.
http://chrysie.tamu.edu/medicago
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                                                                                                                                                                                                                                                                                                                         (bases 1 to 574)
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radixon@noble.org
std Error:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'dev_stage='cell suspensions were subcultured every 14 days. Cells were induced six days after subculture' note="vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 an 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation." a 108 c 125 g 157 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:388
/clone="NF098E01EC"
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/db_xref="taxon:3880"
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Pred. No.
                                                                                                                              Upper Buford Circle,
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M271969e TIGR sequence
MTKAK29TK More information is available at:
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA 9AA CTA 9tg 9AT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       411 Borlaug Hall, 1991 Upper Buford Circle, Tel: 612 625 5715 Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Carroll D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fedorova,M., Pierson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P., C.D., Bowman,C.L., Craven,M.B., Cho,J. and Fraser,C.M. ESTs from senescent nodules of Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                         Department of Agronomy and Plant Genetics University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE997991.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE997991 586 bp
EST429714 GVSN Medicago
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Location/Qualifiers
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114 c 137 g 167 t 1 others
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                                                                    /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pGVSN-8F9"
/tissue_type="senescent root nodules"
/dev_stage="mixture of effective nodules from
                                                 /clone_lib="GVSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month
/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain XLOLR"
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/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pGVN-67F7"
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Pred. No.
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VERSION
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Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK
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1 (bases 1 to 635)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other name: MHAM-7a-F10; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW58472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Harrison M.J.
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21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer: T3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from roots of Medicago truncatula after colonization with
/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host-"E. coli strain xLOLR"
/note="Yector: pBluescript SK; Site_1: EcoRI; Site_2:
xho1; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage" /lab_host="E. coli strain SOLR" /lab_host="E. coli strain SOLR" /note="Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2: XhOI; CDNA was prepared from polyA+ enriched RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The cDNA was directionally ligated into the Uni-ZAP ZR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-ZAP phage-using Ex-Assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                /db_xref="taxon:11
/clone="MHAM-7K19"
                                                                                                                                                                                                                                                                                                                                                                                                  library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                           /clone_lib="MHAM"
                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Medicago truncatula genotype A17"
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Medicago truncatula/Glomus versiforme mixed
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AW584724/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C. Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C. ESTs from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mjharrison@noble.org
Other name: MHAM-7a-F11; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
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h 17.1%; Score 21; DB
Similarity 100.0%; Pred. No. 0.
21; Conservative 0; Mismatches
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580-223-5810
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                                                                                                                                   Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."

163 c 108 g 177 t
                                                                                                                                                                                                                                                      /tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
/note="Yector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
directionally ligated into the Unizap XR vector from
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library"
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159 c 103 g 171 t
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/db_xref="taxon:119092"
/clone="MHAM-7K21"
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AQ597145 444 bp DNA
HS_5240_A1_B11_SP6E RPCI-11 Human Male
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Other name: MHAM-7d-E06; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M. ESTs from roots of Medicago truncatula after colonization with
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Fax: 580-221-7380
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Contact: Harrison M.J.
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/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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/db_xref="taxon:119092"
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Bonaldo, M.F., Lenno
                                                                                                                                                                          BE653345 468 bp mRNA EST 06-S
UI-M-AL1-ahi-c-07-0-UI.rl NIH_BMAP_MCO_N Mus musculus
UI-M-AL1-ahi-c-07-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                           Mus musculus
                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping scanning the human genome proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                            house mouse
                                                                                                                                               BE653345.1
                                                                                                                                                                 BE653345
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Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 Queen Anne Avenue North, Seattle, WA 98109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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Location/Qualifiers
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1 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=816 Col=21 Row=C"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                               GI:9979245
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Primates;
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Pred. No.
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23;
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                                                     Euteleostomi;
; Murinae; Mus
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AQ597171/c
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MEDLINE
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Best Local
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AQ597171.1
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                                                                                                                                                             Hood, L.
                                                                                                                                                                                                                                                                                      numan.
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56 gagggctgcactgactgg 73
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                                                                      Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center
                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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National Institute of Mental Health
700 Propertive Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                               High Throughput Sequencing 
University of Washington
                                                                                                                                                                                                                                                                 1 (bases 1 to 487)
Mahairas, G.G., Wallace, J.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    discovery
Genome Res. 6 (9),
97044477
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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Queen Anne Avenue : (206) 616-3618
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301 443 9890
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/dev_stage="27:32 days"
/lab_host="PH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
nIH_BMAP_MCO_N library is a normalized library constructed
from mouse cortex. The tag is a string of 5 nucleotides
present between the Not I site and the oligo-dT track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lennon and Soares, Genome Research v: /
Tissue provided by Ms. Annie Novakovich,
rahoratories."
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/db_xref="taxon:10090"
/clone="UI-M-AL1-ahi-c-07-0-UI"
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Pred. No.
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                      North,
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                      Seattle,
                                                                                                                                                                                                                                                                      Smith, K.,
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23;
                                                                                               Hood
                                                                                                                                                                                                                                        Young, J.,
                      WA 98109, USA
                                                                                                                                                                                                                                          Swartzell,S.,
g,J., Zhao,S.,
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ORGANISM
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source
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Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 337 row: C column: 12
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                                          Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                   Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Other_GSSs: RPCI-24-337C12.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Russell,D., de Jong,P. and Fraser,C.M. Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 533)
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Location/Qualifiers
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Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B.,
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Plate: 816 row: I column: 23
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                 Location/Qualifiers
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/db_xref="taxon:9606"
/clone="plate=815 Col=23 Row=I"
/clone_lib="RPCI-11 Human Male BAC Library"
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Pred. No.
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23;
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RESULT 20
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (lnf@fresgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 129 row: H column: 21
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Other_GSSs: RPCI-23-129H21.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,B., Levins,M., Mcgann,S.,
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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RPCI-23-129H21.TV RPCI-23
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_2: BamH1; Sites using MboI partially digested male C57BL/6JDNA."
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of ECORI and ECORI Methylase. Size
                                                                                                                                                      /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-129H21"
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                                                                                                             /clone_lib="RPCI-23"
/sex="Female"
                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                      Location/Qualifiers
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/clone="RPCI-24-337C12"
/clone_lib="RPCI-24"
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/strain="C57BL/6J"
                                                                                          /lab_host="DH10B"
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100.0%; Pr
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Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-34A15.TJ
Contact: Shaving Theorem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COntact: Juny 1975
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 34 row: A column: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: szhao@tigr.org
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1. (bases 1 to 595)
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                                                                                                    /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/GJ mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "125 c 74 g 140 t
                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="RPCI-23-34A15"
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                                                                                                                                                                                                                                                                                  'lab_host="DH10B"
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100.0%; Pr
    14.6%;
100.0%;
  Score 18;
Pred. No.
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Pred. No.
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DB 13;
24;
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23;
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                    Length 595;
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DEFINITION
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BF815581/c
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AZ396970 606 bp .DNA GSS 03-OCT-2000 1M0161D13R Mouse 10kb plasmid UUGC1M.library Mus musculus genomic
                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR2&t2=MR2-CI0128-041200-009-c02&t3=2000-12-04&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
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                                                                                                                                                                                                                                                                                                                   /note="Organ: colon_ins; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

a 137 c 151 g 152 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone_lib="CI0128"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
BF208765
                                                                                                                                                                                                18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 016i row: D column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Wright, D., Weiss, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
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(bases 1 to 606)
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                                                                                                                                                                                                                                                                                                                                       147
                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114 jgb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and provided to adaptors of pNA was annealed to
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                                                                                                                                                                                                                                                                                                                                     adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

95 c 107 g 257 t
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                                                                                                                                                                                                                                                                                                                                                                                                                             purified.
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/clone="UUGC1M0161D13"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
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1 (bases 1 to 634)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 167)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kusakabe, M., C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV326766 167 bp mRNA EST 11-NOV-1999 AV326766 RIKEN full-length enriched, adult male medulla oblongata Mus musculus cDNA clone 6330415D21 3', mRNA sequence. AV326766
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BF208765.1 GI:11102351
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                   house mouse.
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/clone_lib="NIH_MGC_3"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: bladder; Vector: pDNR-LIB (Clontech):
Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Site
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/db_xref="taxon:9606"
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17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sughiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
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                                                                                        Conservative
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igemoto,Y., Shiraki,T., Soqabe,Y., Sugahara,Y., Suzuki,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                            3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                                                                                                                                                                                                                                                                                                                                    BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="medulla oblongata"
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                                                                                                                                                                                                                                                                 Local
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AV337137 RIKEN full-length enriched,
CDNA clone 6332414J18 3
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Mus musculus
                                             AV337137.1
                                                             Mus musculus
AV337137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FMAX: 314 AUV 1012
Email: mouseestéwatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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             nouse mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
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(bases 1 to 211)
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="mAGE:1262011"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="whole skin"
/dev_stage="11 weeks old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus
                                             GI:6377189
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100.0%;
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Rodentia;
                                                                                                                                                                                                                                                 0;
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75;
                                                                      3', mRNA sequence.
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                                                                                        adult male medulla oblongata
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki v and Hawashizaki v
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Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 249)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                      prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                    prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="medulla oblongata"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RIKEN full-length enriched, adult male medulla
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BB382343
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
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Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         system.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
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/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike
                                                                                                                                                                          cerebellum"
                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="C230019C09"
                                                                                         /dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                                                                                                                        /clone_lib="RIKEN full-length enriched, 0
                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                               /tissue_type="cerebellum"
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     se Genome Encyclopedia
Research Group in Riken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai (C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, R., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Cohtact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                    Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV277980 296 bp mRNA EST 05-NOV-1999 AV277980 RIKEN full-length enriched, adult male testis (DH5a) Mus musculus cDNA clone 4932703E19 3', mRNA sequence.
AV277980
                                                                                                                                         Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibate, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazak:
                                                                                                                                                                                                                                                                                     Matsuura, S., Carninci, P., Muramatsu, M.,
                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., (
                                                                                                                                                                                                                                                                                                                                                                                                                              1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                 and Hayashizaki, Y.
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FLC I."
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77;
                                                                                                                                                                                                                                                                                     Ozawa,K., Tanaka,T.,
su,M., Okazaki,Y. and
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M., Okazaki
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REFERENCE

AUTHORS

SOURCE ORGANISM

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JOURNAL
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                                                                                                                                                           Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Fukuda, S., Fukunishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, S., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, S., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, S., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, S., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, S., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, S., Suzuki, H., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB248570 296 bp mRNA EST 06-JUL-2000 BB248570 RIKEN full-length enriched, 7 days neonate cerebellum Mus musculus cDNA clone A730026M11 3', mRNA sequence.
BB248570
Unpublished (2000)
                                 ,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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Mammalia; Eutheria;
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                                                                                                    T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yam, Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/clone="4932703E19"
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/strain="C57BL/6J"
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78;
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                                                                          AI466360 301 bp mrNA
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IMAGE:1262011 5', mRNA sequence.
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17; Conser
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Tel: 81-45-503-9222
        house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Researd Sciences Center (GSC), Yokohama Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High-efficiency full-length cDNA cloning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="cerebellum"
/dev_stage="7 days neonat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RIKEN full-length enriched, 7 days neonate
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100.0%; Pr
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78;
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                                                                                                                                                                                                                                                                                                                                                                                                    71 TGCACTGACTGGTAAGT 87
                                                                                                                                                                                                                      sequence.
BI188737
Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,,M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database Unpublished (2001)
                                                                                                                                                                                                                                                    BI188737 316 bp mRNA EST LU-JUL-ZUU1 d2g04fs rl Fusarium sporotrichioides Tri 10 overexpressed cDNI library Fusarium sporotrichioides cDNA clone d2g04fs 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
                                                                                                                     Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                   EST
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1 (bases 1 to 301)
Marra, M., Hillier, L.,
                                                                                                  Hypocreales; mitosporic Hypocreales;
                                                                                                                                                              Fusarium sporotrichioides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-NCI Mouse EST Project 1999
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/clone="IMAGE:1262011"
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/strain="C57BL/6"
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Best Local
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                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                               Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI266425 329 bp mRNA EST 18-JUL-2001 NF097C04IN1F1034 Insect herbivory Medicago truncatula cDNA clone NF097C04IN 5', mRNA sequence.
                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Korth K
                                                                                                                                                                                                                                                                                                           Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A.,,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts No.
                                                                                         Email: kkorth@comp.uark.edu
Insert Length: 329 Std Error: 0.00
Plate: 097 row: C column: 04
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                 University of Arkansas
217 Plant Science Building,
Tel: 501 575 5191
Fax: 501 575 7601
                                                                                                                                                                                                                                     Dept. of Plant Pathology
                                                                                                                                                                                                                                                                                          Medicago truncatula insect herbivory library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
10.072 gi15668770|gb|AAD459 (AC005916) T17H3.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 405 325 4912 Fax: 405 325 7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA.
                                                                                                                                                                                                                                                                                                                                                                                       Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  barrel medic
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Location/Qualifiers
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/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF097C04IN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript" 102 c 63 g 69 t
                                                                         Location/Qualifiers
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/clone="d2g04fs"
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/strain="Tri 10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nc06c06.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007338
similar to contains Alu repetitive element;contains element MER35
repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index .
Unpublished (1997)
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 334)
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                                          /note="Nector: pawp10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10 0.000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pawP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by
                              David Krizman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

a 62 c 50 g 104 t 2 others
                                                                                                                                                                                                                                                                                                                        /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1007338"
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/dev_stage="mature"
/note="Vector: Lambda Zap; Library was produced from fully
                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Pr1"
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C70635 Yuji Kohara unput
Clone yk411b1 5', mRNA s
C70635
C70635.1 GI:2441160
EST.
                                    Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                       BI266362 366 bp mRNA EST
NF092D09IN1F1078 Insect herbivory Medicago
NF092D09IN 5', mRNA sequence.
                                                                                                         EST.
  1 (bases 1 to 366)
Korth, K., Scott, A.D
                                                                                                                    BI266362.1 GI:14870403
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Yata 1111, Mishima, Shizuoka 41
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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                             Medicago
                                                                                           barrel medic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk411b1"
                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Yuji Kohara unpublished
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
63 c 79 g 106 t 10 c
  Scott, A.D.,
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 Harris, A.R.,
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truncatula cDNA clone
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Bell, C.J., Flores
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              The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
                                                                                                                                                                                                                                                                                                                                                         Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
17; Conserv
                                                                                                                                                                                                                              National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: kkorth@comp.uark.edu
Insert Length: 366 Std Error: 0.0
Plate: 092 row: D column: 09
Seq primer: TCACACAGGAAACAGCTATGAC.
clones from RESEARCH GENETICS.
                                                                                                                                                                        Tel: 301 443 1706 Fax: 301 443 9890
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                    Email: mEST@mail.nih.gov
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217 Plant Science Building,
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Contact: Korth K
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69 c 52 g 128 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vector: Lambda Zap; Library was produced from fully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Medicago truncatula"
/db_xref="taxon:3880"
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Pred. No.
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                                        AUTHORS
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                                                                                                                                   Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                                                                                                                                                                    BF649642 456 bp mRNA EST 20-DEC-2000 NF082D01EC1F1012 Elicited cell culture Medicago truncatula cDNA clone NF082D01EC 5', mRNA sequence.
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17; Conserv
                                                                                                                                                                                                                                                                                                                       EST
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   Flores, H.R.,
                                Torres-Jerez, I.,
                                                                                                             Medicago.
                                                                                                                                                                                                                                                                                      barrel medic.
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                                                                     (bases 1 to 456)
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TAG_SEQ=ACGGC"
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/clone="UI-M-BH3-ari--04-0-UI"
/clone_lib="NIH_BMAP_M_S4"
/clone_lib="NIH_BMAP_M_S4"
/dev_stage="27-32 days"
/lab_host="DH10B_(Life_Technologies)"
/lab_host="DH10B_(Life_Technologies)"
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Inman, J.T., Weller, J.W. and May, G.D.
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                                Gonzales, R.A.,
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             The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the hippocampus tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
17; Conserv
                                                                                                                                                                Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                 Contact: Chin, H
                                                                                                                                                                                                                                                                                                                       97044477
                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                               discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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The Samuel Roberts Noble Foundation
2510 Sam Woble Parkway, Ardmore, OK
Tel: 580 221 7302
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Contact: Dixon RA
GENETICS. It should be noted that Bento Soares is
                                                                                                                                                                                                                                6001 Executive Blvd.
20892-9643, USA
                                                                                                                                                                                                                                                  National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC
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/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50uy/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 an
24 hours after induction. Equal amounts of RNA from each
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/db_xref="taxon:3880"
/clone="NF082D01EC"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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100.0%; Pr
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 86 c \, 66 g \, 158 t
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                                                                                                                                                                                                                                                                                                                                                                                 approaches to facilitate gene
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                                                                                                                                                                                 Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                             l (bases 1 to 519)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanns Shoemaker, R., Meim, P., Vodkin, L., Kucaba, T., Martin, J., Beck, C., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurl, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW394535 519 bp mRNA EST 07-FEB-2000 sh32c05.yl Gm-c1017 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1017-3393 5' similar to TR:083191 083191 CONSERVED HYPOTHETICAL
Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN. ;, mRNA sequence. AW394535 AW394535.1 GI:6912947
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TAG_LIB-NIH_BMAP_MHI2_S1
TAG_TISSUE-hippocampus
TAG_TISSUE-TAGTC7
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_MHI2_S1 library is a subtracted library derived from NIH_BMAP_MHI2. NIH_BMAP_MHI2 is a library derived from NIH_BMAP_MHI2. NIH_BMAP_MHI2 is a library derived from NIH_BMAP_MHI2.
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/clone="UI-M-B21-bft-e-20-0-UI"
/clone_1bb="NIHE_BMAP_MHI2_S1"
/dev_stage="27-32 days"
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                              Class: plasmid ends
High quality sequence stop: 526.
Location/Qualifiers
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17; Conserv
                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0467 row: O column: 08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ626769 526 bp DNA GSS 13-DEC: 1M0467008F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0467008 F, DNA sequence.
                                                                                                       Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                         University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                       Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
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                                                                                                                                                                                                                                                         Biomedical Polymers Research Bldg.,
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/organism="Mus musculus"
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/db_xref="taxon:3847"
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/lab_host="XL10-Gold"
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/clone_lib="Gm-c1017"
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OV1_14_H02.g2_A002
                                                                                                                                                                             Email: mmpratteuga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                   The University of Georgia
Plant Sciences Building, Rm. 2502, Athens,
                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                An EST database from Sorghum:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 541)
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                                                                             POLYA=No.
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97 c 92 g 122 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil473214) gblaF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                 Location/Qualifiers
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
/organism="Sorghum bicolor"
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Pred. No.
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VERSION KEYWORDS

COMMENT

TITLE

FEATURES

10.5 kb range using preparative agarose gel

RESULT 4 BG048538

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 tacaaccctgatgacct 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0229 row: L column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2M0229L22R Mouse 10kb plasmid UUGC2M library Mus musculus clone UUGC2M0229L22 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ961481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Islam, H., Longacre, S., Mahmoud, M., Meenen, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
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/clone_lib="Ovary 1 (OV1)"
/clone_lib="Ovary 1 (OV1)"
/clone_lipan: Mix of ovaries of varying immature stages
/note="Organ: Mix of ovaries of varying immature stages
from 8-week-old plants; Vector: pBluescript II from Lambda
Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 111 c 141 g 150 t
was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                          /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biomedical
                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0229L22"
                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                              /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                       /sex="Female"
                                                                                                                                                                                                                                                                          /clone_lib="Mouse 10kb plasmid UUGC2M library"
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100.0%; Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymers Research Bldg.,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 217 row: O column: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Other_GSSs: RPCI-23-21704.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(Pieter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,B., Levins,M.,
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao,S., Nierman,W., Feldblyum,T., Malek,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ561989.1 GI:11241809
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1 (bases 1 to 555)
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            193
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                                                                                                                                                                                                                                                                                                                                                                                                                              BAC ends.
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/GJ mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "108 c 116 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xilo-Gold (Stratagene) cells and selected for ampicillin resistance. "
139 c 101 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="RPCI-23-21704"
                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                  'lab_host="DH10B"
                                                                                                                                                                                                                              'sex="Female"
                                                                                                                                                                                                                                                       clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
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California Institute of Technology
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20402566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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SP_0046_Al_B09_T7 Strongylocentrotus purpuratus, purple sea
sperm genomic BAC library Strongylocentrotus purpuratus geno
clone_Plate=46 Col=17 Row-C, DNA sequence.
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17; Conserv
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Class: BAC ends
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                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                   Email: acameron@caltech.edu
                                                                                                                                                                                                                                                                                                                                                                                                                 Pasadena California 91125,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Cameron,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotidae; Strongylocentrotus.
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(626) 793-3047
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/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
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AC068680 AC007600

Description AC010953

CNS07EFA CNS01RII AC024417 AP001675

AP003046 AL161454 T8K14 AC008790

AC007600 Homo sapi AC003298 Homo sapi AP000958 Homo sapi AP000958 Homo sapi AC024713 Homo sapi AL153612 Human chr AC024417 Homo sapi AL14746 Caenorhabdi AL357912 Human DNA AC027498 Homo sapi AX073208 Sequence AE002395 Neisseria AC006614 Caenorhab AC022128 Homo sapi AC07202 Arabidops AC007202 Arabidops AC007202 Arabidops AC007202 Arabidops AC007203 Homo sapi AC0034225 Homo sapi AC0034225 Homo sapi AC0034225 Homo sapi AC003425 Homo sapi AC003425 Homo sapi AC003776 Homo sapi AC023537 Homo sapi AC024315 Homo sapi AC024315 Homo sapi AC025501 Mus muscu AL357568 Homo sapi AC025501 Mus muscu AC04976 Homo sapi AC025501 Mus muscu AC049756 Homo sapi AC025501 Mus muscu AC049756 Homo sapi AC025501 Mus muscu AC049756 Homo sapi AC025501 Mus muscu AC0499 Sequence AY004261 Heterocab AC006808 Caenorhab AL031353 S. pombe c AC018376 Homo sapi AC018376 Homo sapi

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ALIGNMENTS

NA HTG 28-SEP-1999 LOW-PASS SEQUENCE SAMPLING.

AX044029 AX094499

AC079583

EYWORDS	HTG; HTGS_PHASEO.
DURCE	human .
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
SFERENCE	1 (bases 1 to 69734)
AUTHORS	Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE	Homo sapiens, clone 5_H_9
JOURNAL	Unpublished
EFERENCE	2 (bases 1 to 69734)
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
	Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
	Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
	Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

RE

SUMMARIES

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	gap of unknown length	gap of unknown lend	contig of 877 bp in le	contig of 863 bp in	contig of 934 bp in le	gap of unknown leng	unknown le	contig of 882 bp in l	of 894 b	of 903 b		gap of unknown length	unknown le	gap of unknown length contiq of 879 bp in l	$\sigma$	of 862 b	of 870 b		unknown le	unknown le	contig of 886 bp in l	of 854 b	contig of 874 bp in large of unknown length	unknown le	unknown le	gap of unknown length contig of 885 bp in l	of 865 b	contig of 933 bp in l	rue accession	ompletion.	ps among clones to not be assumed that	that may be gene-r	ich they appear is	sequencing reads that have not been assementings. Runs of N are used to separate t	* NOTE: This record contains 78 individual	hington adm/bar	Street, Cambridge, tified using Repeat	Submitted (28-SEP-1999) Whitehead Institute/MIT Center	nmer, A. and Zody, M	ojanovic,N., Subran ., Vassiliev,H., Vo	V., Riley,R., Roy,l	McKernan, K., McLau	R., Jones,C., Kanı	Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan T Gardona S Grant G Hagos B Heaford A Horton
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TITLE
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                                              Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Cooke,S., Domino,M., Doyle,M., Ferreira,P., FittHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Tliev,I., Johnson,R., Jones,C., Kann,L., Kara, Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J
                                                                                                                                              Homo sapiens, clone RP11-22D13
Unpublished
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 178035)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                       HTG;
                                                                                                                                                                                                                                                                                                    AC068680 178035 bp DNA HTG 04-JUN-2000 HOMO Sapiens clone RP11-22D13, WORKING DRAFT SEQUENCE, 11 unordered
                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                   AC068680.3 GI:8247854
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McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1212: contig of 1212 bp in length
1213 1312: gap of
1318: sap of 4506 bp in length
5818: contig of 4506 bp in length
5819 5918: gap of
100 bp
5919 9462: contig of 3544 bp in length
9463 9562: gap of
100 bp
15212 15311: gap of
100 bp
15212 15311: gap of
100 bp
15312 28255: contig of 12944 bp in length
1836 28355: gap of
100 bp
16314 28255: contig of 16291 bp in length
18464 44746: gap of
100 bp
16316 28356 1646: contig of 16291 bp in length
18464 44746: gap of
1866 bp in length
1861 bp in length
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63410 63509: gr
63510 90494
90495 90594: gr
90595 118529
118530 118629: dr
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Center clone name: 22_D_13
-----Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
                                                                                      145845 145944:
145945 178035
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1. .178035
                                   Location/Qualifiers
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                                                                                                                                                                  63509: gap of 100 bp 10494: contig of 26985 bp in 1090594: gap of 100 bp 118529: contig of 27935 bp in 1018629: gap of 100 bp 118644: contig of 27215 bp in 10186594: contig of 27215 bp in 10186594. contig of 27215 bp in 10
                                                                                 178035: cont
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/organism="Homo sapiens" /db\_xref="taxon:9606"

/clone="RP11-22D13"

/clone\_lib="RPCI-11 Human Male BAC'

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REFERENCE
AUTHORS
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LOCUS
                                                                                                                                          COMMENT
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                                                                                                                                                                                                                   Bruce, D., Mundt, M., Dóggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., McMurry, K., Han, C., and Deaven, L.
                                                   Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
                                                                                                                                  Genome Institute, Los Alamos National Laboratory, MS M888, Alamos, NM 87545, USA On Jul 3, 2001 this sequence version replaced gi:8575868.
                                                                                                                                                                                                Submitted (20-MAY-1999) Center for Human Genome Studies,
                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 183079)
DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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AC007600.4 GI:14589421
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                                                                                                                                                                                                                                                                                                                                                                              Sequencing of Human Chromosome 16
Base-by-base quality values are not generally visible from the
                  Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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90595. .118529
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145945. .178035
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40236 c 39973 g 47951 t
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/note="assembly_fragment
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Pred. No. 0.31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1006 others
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AL UNPUBLIANCE

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AL UNPUBLIANCE

CE 2 (bases I to 194198)

RS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Baldwin,J., Barna,N., Beckerly,R., Boguslawkiy,L., Boukhgalter,B.,

Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,

Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,

Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,

Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,

Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,

McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,

McDwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,

Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tesfaye,S., Tirrell,A., Vassliev,H., Vo,A., Wheeler,J., Wu,X.,

Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens, clone RP11-3N3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
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This entry has been annotated with sequence quality
This entry has been annotated by the Phrap assembly program.
All manually edited bases have been reduced to quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of this entry's ASN.1 file.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality levels above 40 are expected to 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 183079: contig of 183079 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 194198)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTGS_PHASE1; HTGS_DRAFT
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1. .183079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="RP11-264A16"
41752 c 42357 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194198 bp DNA HTG 20-SEP-2000 
ns clone RP11-3N3, WORKING DRAFT SEQUENCE, 19 unordered
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nusbaum, C. and Lander, E.
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0.31;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                              58824 58823: gap of 100 bp

58824 68160: contig of 9337 bp in length

68161 68260: gap of 100 bp

68261 84475: contig of 16215 bp in length

84476 84575: gap of 100 bp

84576 98534: contig of 19359 bp in length

98535 98634: gap of 100 bp

98635 114643: contig of 1600 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 185739 bases at least Q40
Consensus quality: 185725 bases at least Q30
Consensus quality: 191725 bases at least Q20
Consensus quality: 191400 bases at least Q20
Insert size: 194000; agarose-fp
Insert size: 192398; sum-of-contiss
Quality coverage: 5.4 in Q20 bases; sum-of-contiss
Quality coverage: 5.5 in Q20 bases; sum-of-contiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be
e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 16747: contig of 16747 bp in length
16748 16847: gap of 100 bp
16848 18184: contig of 1337 bp in length
18185 18284: gap of 100 bp
18285 21234: contig of 2950 bp in length
21235 21334: gap of 100 bp
21335 23492: contig of 2158 bp in length
2335 23492: contig of 2158 bp in length
23593 2592: gap of 100 bp
23593 26852: contig of 3260 bp in length
26853 26952: gap of 100 bp
                                                                                                                         114644 114743: gap of 100 bp
114744 144676: contig of 29933 b
144677 144776: gap of 100 bp
144677 14776: gap of 15271 b
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Contact: sequence_submissions@genome.wi.mit.edu
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78 30977; gap of 100 bp
78 35870; config of 4893 b
1 35970; gap of 100 bp
1 40691; config of 4091
Location/Qualifiers
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                                                                       0147: gap of 100 bp
178836: contig of 18689 bp in length
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51760: contig of 6756 k
360: gap of 100 bp
58723: contig of 6863 k
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contig of 4721 k
                       contig of 15262 bp in length
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RESULT 5
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   REFERENCE
                                                            SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 50974)
                                           Homo sapiens DNA, clone:B794P4
Homo sapiens
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                                                                                         AP000958.2
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Homo sapiens genomic DNA, chromosor
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84576. .98534
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/db_xref="taxon:9606"
/clone="RP11-3N3"
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58261. .84475
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                                                                                                                                                                                                                                                            Direct Submission
Submitted (01-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 1, 2000 this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 138354 bases at least Q40
                                                                      Mammalia, Eutheria; Primates; Cata
1 (bases 1 to 155304)
Waterston, R.H.
The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome SEQUENCE, 31 unordered p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (17-DEC-1999) to the DDBJ/EMBL/GenBank databases.

Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 50,974 genomic DNA of 21q21.1-q21.2 published Only in DataBase (1999) In press 2 toses 1 to 50974)
                                                                                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
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                                                                                                                                                site:http://genome.wustl.edu/gsc/index.shtml
----- Project Information ------
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/db_xref="taxon:9606"
/chromosome="21"
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Sutheria; Primates; Catarrhini; Hominidae; Homo.
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RP11-170F21, WORKING DRAFT
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Consensus quality: 142506 bases at least Q30 Consensus quality: 144038 bases at least Q20 Insert size: 150000; agarose-fp Insert size: 150578; sum-of-contigs Quality coverage: 3.56 in Q20 bases; agarose-fp Quality coverage: 3.67 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                    100410
100510
                      109406
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69839. .76434
                                               /note="assembly_name:Contig43"
134509. .155304
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                                                                                                                              note="assembly_name:Contig41"
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100510. .109405
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45231. .49657
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37143. .40035
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/db_xref="taxon:9606"
/chromosome="21"
                                                                                                                                                                                                                                                                  note="assembly_name:Contig37"
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1927. .3373
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          embly_name:Contig44"
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                                                                                               The following BAC sequence is oriented from the T7 to the SP6 end. IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc. . even if efforts are made to eliminate these contaminating sequences.
Assembly program: Phrap; version 2.0
Quality coverage: 5.91x in Q20 bases; sum-of-contigs
                                       1 (bases 1 to 158927)
Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Winck Brottlier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguena Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J. Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNSU7EFA 158927 bp DNA HTG 29-MAY-Homo sapiens chromosome 14 clone R-326E7, *** SEQUENCING PROGRESS ***, 2 ordered pieces.
                                                                                                                                                                                                                                                                                           Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                       Center code: GS
                                                                                                                                                                                                                                                                                                                                                        Center: Genoscope / Centre National de
                                                                                                                                                                                                                                                                                                                                                                                               Percentage of bases with a quality value >=
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On Apr 4, 2001 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-MAY-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT.
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36142
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100.0%; Pred. No.
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                                                             R-346L24 (AC=AL163612)
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                                                                                               AUTHORS
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Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 171345)
Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J.

Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                   CNS01RII 171345 bp DNA PRI 28-APR-2001
Human chromosome 14 DNA sequence BAC R-346L24 of library RPCI-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contigs composition:
98062 bp contig from 98163 to 158927.
60765 bp contig from 98163 to 158927.

* NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
tare represented as runs of N. The order of the pieces
to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                      HTG
                                                                                                                                                                                                                                                                             from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                             numan
                                                                                                                                                                                                                                                        AL163612.5 GI:13276126
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1 98062: contig of 98062 bp in length
98063 98162: gap of 100 bp
98163 158927: contig of 60765 bp in length.
Location/Qualifiers
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RHdb:RH95620
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note="matching EMBL:Z23897"
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RHdb:RH53692
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/db_xref="taxon:9606"
/chromosome="14"
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ORGANISM
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KEYWORDS
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AC024417
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ORIGIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 182340)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 4, clone RP11-221C21

    Web: www.genoscope.cns.fr)
    On Mar 12, 2001 this sequence version replaced gi:11875958.
    ------ Genome Center

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The following BAC (overlapping the SP6 end): R-649E7 (AC-AL139099)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26-APR-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
                                                                                                Homo sapiens
                                                                                                                                    AC024417.2 GI:7229920
HTG; HTGS_PHASE1.
                                                                                                                                                                                          ACO24417 182340 bp DNA HTG
Homo sapiens chromosome 4 clone RP11-221C21
IN PROGRESS ***, 64 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 2.0 Quality coverage: 9.09x in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Genoscope / Centre National de Center code: GS
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Direct Submission
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/db_xref="taxon:9606"
/chromosome="14"
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/clone_lib="RPCI-11"
35560 c 32962 g 47288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 12, 2000 this sequence version replaced gi:7108213.
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Birren, B., Linton, L.,
Anderson, S., Baldwin, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
8866 8965: gap of 1238 bp in 8966 9989: contig of 1024 bp in 9990 10089: gap of 100 bp 10090 11332: contig of 1243 bp in 1133 11432: gap of 100 bp 11433 11432: gap of 1165 bp in 112598 12697: gap of 100 bp 11698 13979: contig of 1262 bp in 11980 14079: gap of 100 bp 13980 14079: gap of 100 bp 1544: contig of 1465 bp in 161545 15644: gap of 100 bp 15645 17090: contig of 1446 bp in 1617091 17190: gap of 100 bp 17191 18508.
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Center clone name: 221_C_21
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1156 2524: c
2525 2624: gap c
2525 3768: c
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7628
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35 burrely apport 4328 by ...
49 62876; contig of 2328 by ...
577 62676; gap of 100 bp
2677 64748; contig of 2072 bp in length
4749 64848; gap of 100 bp
34849 65725; gap of 100 bp
67526 70617; contig of 3092 bp in length
70618 70717; gap of 100 bp
70718 72665; contig of 1948 bp in length
72766 7275; gap of 100 bp
72766 75102; contig of 2337 bp in length
75103 75202; gap of 100 bp
75203 75445; gap of 100 bp
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81498 81497; gap of 100 bp
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88847 88946; gap of 100 bp
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43402 43501: gap of 100 bp
43502 44790: contig of 1289 bp in length
44791 44890: gap of 100 bp
44891 46931: contig of 2041 bp in length 36847 36947 35186 30047 19830 19930 96847 96946: 35086 33475 30147 28912 28812 28911: 21214 21313: 114 57694: contig of 2381 bp 695 57794: gap of 100 bp 695 57794: gap of 100 bp 795 60148: contig of 2354 bp i 96248: gap of 100 bp 62576: contig of 2328 bp ic 7 6676: gap of 100 bp 64748: contig of 2328 bp ic 64748: contig 7 30146: gap of 100 bp 17 31304: contig of 1158 bp in length 17 31304: contig of 1158 bp in length 17 31404: gap of 100 bp in length 17 33574: gap of 100 bp 17 3574: gap of 100 bp 18 35085: contig of 1511 bp in length 18 36846: contig of 1661 bp in length 18 36946: gap of 100 bp 1947 38786: contig of 1840 bp in length 1947 3 17 93512: contig of 4566 k 13 93612: gap of 100 bp 13 93646: contig of 3234 k 17 96946: gap of 100 bp 17 99557: contig of 2611 k 1 22808: contig of 1495 1 22908: gap of 27262 99657: 19929: gap of 21213: con 24634: 18608: 24534: contig of 1626 bp i. 24534: gap of 100 hr 2755 100 bp 10 con 28811: 99557: contig of 2611 557: gap of 100 b 102370: contig of 2713 2470: gap of 100 b 08: gap of 100 b 19829: contig of 1221 contig of 1284 100 bp 1611 bp in 100 bp 107354 bp in 100 bp 1081 bp in 100 bp f 2713 b gd þ đđ фþ bp in in 'n Ín in length Length length length length length length Length length

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AUTHORS
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                          and sequencing cons
Nature 405 (6784),
20289799
                                                       The DNA sequence of human chromosome and sequencing consortium
                                                                                                                                                                                                                                     AP001675 340000 bp DNA
Homo sapiens genomic DNA, Chromosome
AP001675 AL163220 BA000005
AP001675.1 GI:7768691
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/chromosome="4"
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137354: gap of 100 bp

143801: contig of 6447 bp in 16

143901: gap of 100 bp

148857: contig of 4956 bp in 16

148957: gap of 100 bp

156188: contig of 7228 bp in 16
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AL163220: Submitted (10-Apr-2000).
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info.genome@gbf.de
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* e.mail: nshimizu@dmb-med.keio.ac.
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URL: http://www.dmb.med.keio.ac.jp/
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URL: http://hgp.gsc.riken.go.jp/
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                                                                                                                                                                                                   complement(1510. .1686)
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The sequence of C. elegans cosmid T18H9
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Caenorhabditis elegans
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Eukaryota, Metazoa, Nematoda; Chromadorea; Rhabditida;
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The C. elegans Sequencing Consortium.
Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coding sequences below are predicted from computer analysis, using the program Genefinder(P). Green and L. Hillier, ms in preparation).
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Direct Submission
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yk359d10.3, yk359d10.5, yk360d4.3, yk360d4.5, yk363b8.3,
yk363b8.5, yk431e10.3, yk431e10.5"
                                                                                                                                                                                                                                                                                                                                                                                                                      YTBFIRKTLMENLDINVDDVVYVGPYYYMEDKNGIHDMDWTAFWAMAIVWLLIMSSAV
TVFICGYGCYKKITKGLEVSSNSKQTKSJQKOLFYALVVQSAIPFLLMYIPSTVYLFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVSMNVFALHFLYRYATLFPKSKKLFDGARIIFWLTVPQIYGVVWLVTYYAVFRESPE
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1931. .2097,2141. .2338))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1034. .2338)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Bristol N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ∕organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       one m13 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEIGHBORING COSMID INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinxton Hall
      1 protein T18H9.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  St.
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CAGKIFLSSCYSQAPEIVDDRDKQKKNVEDSEDETETDYDDVGDELNEMPSARSGRHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(17485. .20529)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVLKYGILEDMIIGGEDEDLYNQEQILHSKRKYYREFTKSAKEIILCSPYTKFTAPTN
FAQCNNYIQSYVNCFSTKCYYCKKHLRQFMPPTVVTRESSPIICHKLCLMSQVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQLFYKLQEAMDERTVIEKNIIAVSETFRQNAVHAPRVSRLSVPPPLKFSKHVEDANK
GVFLAMDAVMNKTRGDLTWRFKRISHPCFRNSKSLIEVHYCARRPNSEKEFVPCMKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STAGNPAAGRPILTLPSNTTEKHVIALNQWAEVMKSKLEKMRQKSKKALDESMKEHST
MEDLSRAREALSEMGNMYYELNRAAALKCRYNAVFDKRPLYKAVESSIQDLRQKDESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(13055. .13151,13216. 14233. .14463,14508. .14588,15197. .]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(13055. .15649)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPYQNQNQIQNQNQYSNYYRTPSLSRGTDSRPVSTATDTDQTKKQSMSTFK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APK I EEREQWWP AY PSLVNP I NPWRY RDENQANALRWRRALGANVDNS I ATQDLMEKL
LPQNAHMRPSDDELLNRQP I AVQASY I DDESDGKLKNEEKQNQQNATQPPYCYTNQNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLQGALRFHRRLQKKQIRPHRFLMLFNLPYSAFFYTAMYLCTKFFYLANVCLQLMFMN
RFLETDKYKWYGMGALVDLLNGTTWEQSGMFPRVSLCDFDVRVMGNMQEHTIQCVLVI
NIFNEKIFILLWFWYLALLVFTFGSFFYWLLVSLWRHLNVRFIIRHLEMSDIAFDSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QFGGKPVECLVPDIFSSSWEQYAENYCWASDTYYVPTNEPVAGLQSDEKRQRKISYYQ
WVPFFLLLEAACFRLPSLLWKYLAGHSGIKINEIVKLSSDPNNIKPDIKRANIKSLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to C. elegans unc-7 and drosophila ogre and shaking-B proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(8267.
10307. .10562,10610. .
/gene="T18H9.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(8267. .10741)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QITPPFINAINQNLVDLPLFTVFLEHEGDQNGVQGGVYTYGGIDTKNCGPVIAYQPLS
SATYYQFKMSAIGSGSYHSSKGWQVISDTGTSLIGGPKAYVSAIADAVGATWRDDYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĎAGGATNLFILLALVAAALAAVVQVPLVKIEPYRNRLIREGRWVQYRKDREIRREMMN
KQSNDMSVGQYVNDYEDEAYVGNITIGTPQQOFKVILDTGSSMLMIPDITCGTKPENC
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QNCAKVKQYHPLTTGAAYQFYMTSVSSGAYSARNGWTALSDTASSIIYGPKAIVAGIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="T18H9.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MQSNQQPTTSANASGPSGARISSGNIPHSQSMPVLQSGNTANRP/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MVLAAVLSMLRYVGGSDDRDFVDRLHSYFTCNLLIGLAVLVSFK/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="inx-10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MPIYSKLLKEGKWSDYKLQQDQLRSDAYAAGVDDYEHAGYVGKI"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GI:1118134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .8552,8994. .9387,9436. .10047, .10741))
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.15649))
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gene

gene CDS

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SOURCE
ORGANISM
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23408 TTATCTTCAATTTATTCCA 23390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 ttatcttcaatttattcca 116
                    corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 15, 2001 this sequence version replaced ai:8569972
                                                                                                                                                                                                                                                                                                                                                                                                                     During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gi:13751415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG
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AL357912.10 GI:1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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RPQFVRPVRPYTAGRLTPGPPIAPVTOGYSERPPATVAPYIERPVPARPTPYIERPVP
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RPYVAPSTTTQRY I EPTTQRPTTRRATTKR I TTTTTAAPTTPRLTTARATTPLATTSR
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ESVISKTDGSSPPHSPQLRNVDGQELNNDFWPNNPVPQSSQYSYGSDFPPSSSNTTPN
SKKDTAKVTIKAHFKTLLVSRSPSSGSLSLTYLKEKRKDKMLQKLGMKKGQKQKPEEG
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VINRIQNFCHSNSSNPPLTIVGIIGTDKLFSQVVKAYVECLAHKSLANLVNHLRFVAI
PSTSSLFYKMIEGIDPQLDNLCRDLWDRFGDMTLPEKTSLANKIAAWPNSVSSSKMNM
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/note="grd-6"
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5.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone RP11-328N1 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-328N1 is at 1 in this sequence. true left end of clone RP5-1102M4 is at 129958 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/HGP/Chrl
RP11-328N1 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.chori.org/bacpac/home.htm
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29487. .29592
                                                                                                                                                                                                                                                                                                                           /note="MLT2B repeat: 21183. .27754
  /note="LTR8
33523. .338
                                                                                                                                                                                                                                                                                   /note="L1MA3 repeat: matches -1387. .5378 of consensus"
27850. .27996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L1M4 repeat: matches 3258. .3689 of consensus" 1871. .2174
                                          32682.
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1. .130057
                                                                                                                                        /note="L2 repeat: matches 1335. .1441 of
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29211. .29319
                                                                                                                                                                                                                                                                  note="L1M1"
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/note="AluSx repeat: matches 1. .291 of consensus"
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/note="L1ME1 repeat: matches 5814. .6123 of consensus"
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/note="L1PA15 repeat:
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/note="L1M4 repeat: matches 3689.
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/note="AluSq repeat: matches 1. .306 of consensus"
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3. .166
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/chromosome="1"
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"LTR8 repeat: matches 1. .691 of consensus" .33812
                                          .33408
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                                                                                                                                                                                                                                                                repeat: matches 238. .386
                                                                                                                                                                                                                        matches 2064.
                                                        matches 1.
                                                                                                                                                                                                                                                                                                                                                matches 1. .448 of consensus"
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                                                                                                                                                                                .1795 of consensus"
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                                                                                                                                                                                                                              /note="AluYa5 repeat: matches 1. 69724. .69811
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/note="TIGGER1 repeat: matches
                                                                                                                                'note="L1M4 repeat:
                                                                                                                                                                    /note="LlMA6 repeat:
                                                                                                                                                                                                              note="MLT1C
                                                                                                                                                                                                                                                                                     note="MLT1C repeat:
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68960. .69182
                                                                                                                                                                                                                                                                                                                                                                                                note="L1
                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MER5A repeat: matches 1. .183 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1PA13 repeat: matches 3326. .5397 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Alusg repeat: matches 1. .303 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="AluSx repeat: matches 1. .293 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L1PA11 repeat: matches 880. .951 of consensus"
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/note="L1MA7 repeat: matches 5815.
34305. .34552
                                                     'note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                                                           'note="MLTIC repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSx repeat: matches 38. .285 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L1PA13 repeat: matches 5397. .6156 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MER44A repeat: matches 57. .330 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L1PA3 repeat: matches 1596. .3569 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="L1PA11 repeat: matches 951. .6163 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e="TIGGER1 repeat: matches 1.
                                                                                                                                                                                  .70787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .51676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .50428
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                                                                                                                                                                                                                                                                                                           .69415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 54 L 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .61408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .50356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 1740. .1982 of
                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 4640. .5052 of consensus"
                                                                                         repeat:
               repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches -1422. .750 of consensus"
                                                                                                                                matches
               matches
                                                                                                                                                                      matches 6027.
                                                                                                                                                                                                            matches 16.
                                                                                                                                                                                                                                                                                                                           matches 234.
                                                                                           matches 4311. .6108 of consensus"
                                                                                                                                                                                                                                                                                     matches 124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matches 1. .267 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aa 72% conserved'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71% conserved"
                                                                                                                                2938.
               3594. .4311 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .308 of consensus"
                                                                                                                                                                                                            .124 of consensus"
                                                                                                                                                                                                                                               .307 of consensus"
                                                                                                                                                                                                                                                                                                                           .466 of consensus"
                                                                                                                                .3264 of consensus
                                                                                                                                                                                                                                                                                                                                                               .5531 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .60 of consensus"
                                                                                                                                                                                                                                                                                     .226 of consensus
                                                                                                                                                                    .6183 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2278 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .6289
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REFERENCE
AUTHORS
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AC027498/c
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                                                                                                                                                                                                                                                                Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazaares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Medurin, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Peterson, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., P., Rogov, P., Rothman, D., Rogov, P., Rogov, P., Rothman, D., Rogov, P., Rothman, D., Rogov, P., Rogov, P., Rothman, D., Rogov, P., Rogov, P., Rothman, D., Rogov, P., Rogov, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Collins, S., Campopiano, A., Coastle, A., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Dodge, S., Domino, M., Doyle, M., Ferreira, P.,
                                                                                                                                   Roy,A., Santos,R., Schauer,S., Severy,P., Spencër,B., Stange-Thomann, M., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome SEQUENCE, 25 unordered p
                                      Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galagan, J., Gardyna, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C. and Lander, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 18, clone RP11-656L11
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                    Young, G., Zainoun, J., Zimmer, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 180911)
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/note="THE1B-INTERNAL
consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88550.
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/note="L1PA4 repeat: matches 11.
320 Charles Street, Cambridge, MA 02141,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluS repeat: matches 222.
88499. .88549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88763.
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88763. .89267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="THE1B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180911 bp
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18 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ginde, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat:
                                                                                                       and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goyette, M., Graham, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .287 of
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                                                                                                                                          Ye,W.J.,
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COMMENT

Research,

On Apr 20, 2000 this sequence version replaced gi:7342242.

repeats were identified using RepeatMasker: t, A.F.A. & Green, P. (1996-1997)

length length length

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587 29686: gap C.

687 34675: contig of 4yoy C.

1676 34775: gap of 100 bp

4776 39152: contig of 4877 bp in length

49153 39252: gap of 100 bp

44143 44242: gap of 100 bp

48562 48661: gap of 100 bp

48562 48661: gap of 100 bp

48662 53987: contig of 5326 bp in length

53988 54087: gap of 100 bp

53988 54087: gap of 100 bp

60472 60471: gap of 100 bp

60472 67910: contig of 6284 bp in length

60372 60471: gap of 100 bp

68011 74138: gap of 100 bp

68011 74138: gap of 100 bp

74139 74238: gap of 100 bp

80143 80242: gap of 100 bp

80143 80242: gap of 100 bp

80143 80372: contig of 5904 bp in length

8061 88160: gap of 100 bp

80637: contig of 6938 bp in length

80608 700737: gap of 100 bp

10074737: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9065: contig of 2817 bp in length 9066 9165: gap of 100 bp 9166 13447; contig of 4282 bp in length 1348 13547; gap of 100 bp 13548 17515: contig of 3968 bp in length 17516 17615; gap of 100 bp 17616 21812; contig of 4196 bp in length 21812 21911; gap of 100 bp 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 182000; agarose-fp
Insert size: 178511; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reassembly program: Phrap; version 0.960731 Consensus quality: 165132 bases at least Q40 Consensus quality: 173168 bases at least Q30 Consensus quality: 176502 bases at least Q20 Consensus quality: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: L8451
Center clone name: 656_L_11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research
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2416 6148:
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20026: contig of 4115 bp in 1

127 26126: gap of 100 bp

27 29586: contig of 3460 bp in 16

17 29686: gap of 100 bp

34675: con+17
100 bp
100 bp
115083: contig of 10246 bp in length
124831: contig of 9748 bp in length
124931: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2315: contig of 2315 bp in length
5: gap of 100 bp
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of 3733 bp in length
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Best Local Similarity
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136858 136957: gap of 100 bp
136958 150860: contig of 13903 bp in
150861 150960: gap of 100 bp
150961 180911: contig of 29951 bp in
                                                                                                                                                                                                                                                                                                                                                                                                              vector_side:right"
136958. .150860
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150961. .180911
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/db_xref="taxon:9606"
/chromosome="18"
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33104 c 32922 g 54339
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124932. .136857
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AX073208/c
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Best Local S
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                                                                                                       JOURNAL
MEDLINE
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2 (bases 1 to 11018)

Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C.,
Nelson,K.E., Eisen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F.,
Dodson,R.J., Nelson,W.C., Gwinn,M.L., DeBoy,R., Peterson,J.D.,
Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R
                                                                                                                                                                        Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C., Nelson,K.E., Eisen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F., Dodson,R.J., Nelson,W.C., Gwinn,M.L., DeBoy,R., Peterson,J.D., Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R.D., Dougherty,B.A., Mason,T., Ciecko,A., Parksey,D.S., Blair,E., Cittone,H., Clark,E.B., Cotton,M.D., Utterback,T.R., Khouri,H., Qin,H., Vamathevan,J., Gill,J., Scarlato,V., Masignani,V., Pizza,M., Grandi,G., Sun,L., Smith,H.O., Fraser,C.M., Moxon,E.R., Rappuoli,R. and Venter,J.C.
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Sequençe
                                                                                                                           Science
                                                                                                                                           strain MC5
                                                                                                                                                           Complete
                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis MC58.
Neisseria meningitidis MC58
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          the complete genome. AE002395 AE002098
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Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                       Neisseria
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                                                                                                                           287
                                                                                                                                                         genome sequence of Neisseria meningitidis serogroup B
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319 from Patent WO0102550.
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/db_xref="taxon:5476"
197 c 196 g 422 t
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Fleischmann, R.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-MAR-2000) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., B. Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="beta-phosphoglucomutase"
/protein_id="AAP40831.1"
/protein_id="AAP40831.1"
/db_xref="G17225613"
/db_xref="G17225613"
/translation="MTFTAVLEDLDGVITDTAEYHYRAWKKLAEELGISIDRKFNEQL
KGVSRDDSLKRILAHGGKTVSEAEFAELTRRKNDNYVEMIQAVKPEDVYPGILFLLEA
LRANGKKIALASASKNGPFLLERMGLTHFFDAIADPAAVAHSKPAPDIFLAAAEGVDA
                                                    AQGGIAAAWSGEDDIEKHVADTLEAGAGLCDEAAVRAILSQGKPAIEWLLAQGVAFDR
NHNGLHLTREGGHTCRRIAHVADYTGEAVMQSLIAQIRRRPNIRVCERQMALDIQTES
                                                                                                                                                 /product="1-aspartate oxidase"
/protein_id="AAF40832.1"
/db_xref="GI:7225614"
                                                                                                                                                                                                                                                                                             similarity; putative"
                                                                                                                                                                                                                                                                                                                            /note="similar to GB:D13169
PID:42077 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                         complement (3262.
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/gene="NMB0392"
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SGR"
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QGLAGALYPMVTFTGIECHNEWEITFEEIHRNGAIPYAIYNYTNYTGDEGYLAKEGLE
VLVEVSRFWADRVHFSKRNGKYMIHGVTGPNEYENNINNWYTNTLAAWVLDYTREAL
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TFAGSFKALGGSQTDWQVSNSFESEVGSTPETFEKRVIVTTSRDYQSLEAVKAAGRAL
SEKIAGVAFETLLDAHKAGWLHRWEIADVVIEGSDEAQQGIRFNLFQLFSTYYGEDAR
VGNLEFIQFHPTGLARPSENGRTFLISEAVRGEGGILTNQAGERFMPHYDRRAELAPF
                                                                                                                                                                                                                                                                                                                                                                                          /gene="NMB0392"
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/gene="NMB0391"
/note="similar to PID:1495997 percent identity:
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2419. .3084
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PLNQKWSWDKILRSPFIKQADVLQGIYFFSDRFNIDEKRRNFDFYEPMTVHESSLSPC
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akndvagfsveldwqhgvlrrsftvfgvrfnvckflsvaqkelavirweavsvdgkth
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148. .2406
                                                                                                                  /translation="MQTDCDVLIAGNGLAALTLALSLPESFRIVILCKNRLDDTASRH
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                                                                                                                                                                                                                                                                           /codon_start=1
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VNHRWGLDDAVLIKDNHLAYCGSIAQAVQQAKQAVGALTCVEIEVDTLAQLDEAIAAG
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NEFKGGELAALKAEHPEAVVLVHPESBQSVIELGDVVGSTSKLLKAAVSRPEKKFIVA
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                                                                                                                                                                                                                                                                                                        putative"
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LCWGVEPENWSEEYVLQRYEMLYESGLIAEAAEPQANFDFALTGQPMRHDHRRVLATA
LSRLRAKIKYRPVIFELMPPEFTLLQLQNSVEAISGRLLHKQNFRRQIQQQNLIEPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="conserved hypothetical protein; identified by
Glimmer2; putative"
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LLDRKLGEAAKLPLQRMLDFAAGLKKKDVFNGMGPA"
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/gene="NMB0394"
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/gene="NMB0393"
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AIAQLQLWKQNQAEPHTASEYENRNLLECSLAVAQAAYRRRQNIGAHFNSDC"
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PVQHYTCGGIQTDPCGRTSLPQLYALGETACTGLHGANRLASNSLLECVVTARLCAQA
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/gene="NMB0396"
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identified by sequence similarity; putative"
                                                                                                                                                                                                                                                         transl_table=11/
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identity: 67.53; identified by sequence similarity;
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                                   Submitted (01-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                           Waterston, R.H.
Direct Submission
                                                                                                                                     University MO 63108, U
                                                                                                                                                                             Submitted (23-FEB-1999)
                                                                                                                                                                                                                3 (bases 1 to 33803)
Waterston, R.H.
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8685. .8972
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                                                                                                                                                        Sequencing Center, Washington 4444 Forest Park Parkway, St.
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and the Sanger Centre,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
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Direct Submission
Submitted (08 MAR-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 33803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-MAR-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTES:
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TVQQPVNTIYKNKCILKHPIFBQSEPVCGNGVLENGEDCDCGLPGRCSDLNCQPHTCR
FFMHPFFLVLVLASFVAFLVIATWFIVERTYTGYLCFKMYKSKHDRGRASPYTMGQI
GILAASFYQNKKMSH8SIGSNYTILVSNDSFRGYMINCFKMYKSKHDRGRASPYTMGQI
GQQYETTKVFGSYRESFYDDFSDDEFEEQEVPSAYPLPFQVPTCPAYPPNVPINRVTQ
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QTNRGDLSLQSFHEYRNSRLHKLPDHEFATLISYKYAGGLAYVNGMCSSHSVSLSGFY
PNEPRAMGSIFFHEVAHLVGVPHRAVNESIYVPNCLCTPKDSLKEDGCLKIPGFDHDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains similarity to Pfam family PF00200 (Disintegrin), score=15.2, E=0.00052, N=1; coded for elegans cDNA yk228a1.5; coded for by C. elegans cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(8252. .16090)
/gene="C34H3.1"
/gene="C36H3.1"

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Cambridge CB10 IRQ, England
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                    translation="MRKLSIILVFSCIFFNVVSTLEQKHIEYGAAVWGAKAPDYSLAS/
                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAF39762.1"
/db_xref="GI:7206602"
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/chromosome="X"
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/strain="Bristol_N2"
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                                                                                                                                                                                                                                                              Submitted (30-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Mar 30, 2001 this sequence version replaced 91:7711703. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (26-JAN-2000) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
                                                                                                                            Estimated Total Number of Errors is 0.1.
Note: Consensus clipped at overlap with AC008790.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       3\, (bases 1 to 34128) DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                      www-shgc.stanford.edu
Quality: Phrap Quality >=40 99:8% of Sequence;
                                                                                                                                                                                                                         www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 34128)
DOE Joint Genome Institute.
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/protein_id="AAF39763.1"
/db_xref="G1:7206603"
/translation="MLPWQRQVPTSIFPQSNEQVFRMMLAQQHLQLQNFLQQRKMALL
/translation="MLPWQRQVPTSIFPQSNEQVFRMMSPTLTTAAVRPFVPYDQ
AMNPEIPMITDLKKAKFDFTHMADSIESEQKIKEESVSPKMSPTLTTAAVRPFVPYDQ
PWFMIPGRGRTTGRAARPKKEFICKYCDRHFTKSYNLLIHERTHTDERPYSCDVCGKA
                 /clone="CTD-2170G13"
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/chromosome="5"
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/gene="C34H3.2"
                                                                                         /organism="Homo sapiens"
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100.0%; Pr
100.0%; O;
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Query Match

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                                       Worley,K.C.
Direct Submission
Submitted (07-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 57000)
Direct Submission
                                                                                                                                                                                                                                                                                                               Direct Submission
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1 (bases 1 to 57000)
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sapiens 12g BAC RP11-139B1 (Roswell Park Cancer Institute
BAC Library) complete sequence.
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Submitted (23-MAR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Mar 23, 2001 this sequence version replaced gi:13173525. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,

unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:338-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rates than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

## QUALSTAT-REPORT-----

Number of N's in consensus :	Number of consensus changing edits:	Fraction of Phrap values less than 40 :	Average error rate (BCM-Phrap estimate):	Phrap values in estimate:	Contig length:	Summary Statistics
0	306	0.00374019	4.07525e-05	156142	156673	

14543 14545 14549 14550 14551 14553 14553 14555 14556 14563 14563 Position nntgnnnann(n)nccccntntn ntgnnnannn(n)ccccntntnn nannnncccc(n)tntnnnnat nnnnccccnt(n)tnnnnatnn nccccntntn(n)nnnatnnncn nnccccntnt(n)nnnnatnnnc nanntgnnna(n)nnnccccntn
anntgnnnan(n)nnccccntnt ccnanntgnn(n)annnnccccn atconanntg(n)nnannnnccc tccnanntgn(n)nannnncccc tccatccnan(n)tgnnnannnn ctccatccna(n)ntgnnnannn tgctccatcc(n)anntgnnnan aaaggtcttt(n)agttttctct tctcttgttt(n)tccacgtttt Original+Context -- Consensus changing edits cctagatgtg(a)atcatcccct
tagatgtgaa(t)catccccttg
agatgtgaat(c)atccccttgt
gatgtgaatc(a)tccccttgtc
atgtgaatcca(t)ccccttgtct
aatcatcccc(t)tgtctagcat
tcatcccctt(a)tctagcatat atcctagatg(t)gaatcatccc tcctagatgt(g)aatcatcccc atccccttgt(c)tagcatatcc tgctccatcc(t)agatgtgaatcactccatccta(g)atgtgaatca tccccttgtc(t)agcatatcca tccatcctag(a)tgtgaatcat tctcttgttt(c)tccacgtttt aaaggtcttt(g)agttttctct Edited+Context

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Matches
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-JAN-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA-94710, USA On Jan 5, 2001 this sequence version replaced gi:4713943. This sequence is of BAC T8K14 from Arabidopsis thaliana chromosome 1. In order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide overlap between overlaping submitted clones. The 3' end of this sequence overlaps by 2000 bp the 5' end of the sequence of the YAC YUP8H12R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-MAY-1999)
St., Albany, CA 94710, U
5, (bases 1 to 80374)
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Submitted (03-APR-1999) Pl
Street, Albany, CA 94710,
3 (bases 1 to 80374)
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AC007202
AC007202.3
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Submitted (29-APR-1999) P.
Street, Albany, CA 94710,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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join(448. .3246,
4156. .4303,4397
                                                                                                                                                                       Ls a member of the PF|00069 Eukaryotic protein kinase family. ESTs gb|T46484, gb|AF066875 and gb|N96 come from this gene."
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{	t SISDMDDALLGVNKNDGDSEFQYVVAVNGMDIGSGKNSTLLGLDSSSANNLAELDVRN}
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                                                                                                                                                                                                                                                                                                                                                                 448. .5132
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis
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.4303,4397. .4519,4737. .48
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.4824,4933. .513
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EGVAKFLKPSVAGFLMOKELDYLVGAVANPKKFFAATVGGSKVSTKIGVIESLLNTVD
ILLLGGGMIETFFYKAQCLSVGSSLVEEDKLDLAKSLMEKAKAKGVSLLLPTDVVIADK
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AVPTIKYLMGNGSRVVLCSHLGRPKGVTPKYSLKPLVPRLSELLGVEVVMANDSIGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Is a member of the PF|00162 Phosphoglycerate kinase family. ESTs gb|N38721, gb|T22178, gb|R90345, gb|R90715, gb|R913140, gb|R46295, gb|H37082, gb|R46076, gb|R37132, gb|AA597649, gb|AAI100648 and gb|Z48462 come from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   уудп(д1693. .11887,12188. .12265,12354. .12614,12703. .13020,
13129. .13287,13447. .13641)
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GFPLEYIVDIPLDPYLFETICNAGVEVDLLQKRQIHYFMKVFIALLPGILILMFIRES
AMLLLITSKRPLYKKYNQLFMAYAENFILPVGDVSETKSMYKEVVLGGDVWDLLDEL
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SEEFGAMVENLRTPDSEPKDEKTETRHAALPPLGSEFFDYSGLOIKNEDLEELRELGS
GTFGTVYHGKNRGSDVAIKRIKKSCFAGRSSEQERLTGEFWGEAEILSKLHHPNVVAF
YGVVKDGPGGTLATVTEYMVDGSLRHVLVRKDHLDRRKRLIIAMDAAFGMEYLHSKN
TVHFDLKCDNLLVNLKDPSRPICKVGDFGLSKIKRNTLVSGGVRGTLPMMAPELLNGS
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GKSHDEFKTVNDDANHHTHKDVETIFEKVGVSDETLESEPLHKIVNPDDANKNRVVNG
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KNLAEDIDFGKANIRNLVNEAAIMSVRKGRSYIYQQDIVDVLDKQLLEGMGVLLTEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(5680. .11012)
/gene="T8K14.2"
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TVRPYPHDGAAVSMNVQNHDRKNWSYFQQLAEDQFIQRDVVLDQADSRIPSDRKDGGE
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LPPSRDPRQNTTAKPATYRDAVITGQVPLSGIEDQLSTSSSTYAPVHSDSESNLIDLN
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KSGAAKINEMFSIARRNAPAFVFVDEIDAIAGRHARKDPRRRATFEALIAQLDGEKEK
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LGVSGEIGDSYGNWRERLATWKEMLEREKLSEQLNSSAAKYYVEFDMKEYEKSLREDV
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LMEECWAPNPMARPSFTEIAGRLRVMSSAATSTQSKPSAHRASK"
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DEFINITION
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Homo sapiens chromosome
AC008790
AC008790.6 GI:10044330
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18; Conserv
                                                                                  AC008790
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19928. .20028,20158. .20280,20369. .20468,20547. .20693,
20774. .20834,20925. .21022,21110. .21252,21361. .21444,
21529. .21618,21702. .21756)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/protein_id="AAD30223.1"
/protein_id="AAD30223.1"
/protein_id="AAD30223.1"
/db_xref==01:4835756"
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RIATSRDDIEVVAVNDPFIDAKYMAYMLKYDSTHGRFKGSINVIDDSTLEINGKKUVL
RIATSRDDIEVVAVNDPFIDAKYMAYMLKYDSTHGRFKGSINVIDDSTEINGKKUVL
VSKRDPSEIPWADLGADYVVESSGVFTTLSKAASHLKGGAKFVISAPSADAPMFVVG
VNEHTYQPNMOIVSNASCTTNCLAPLAKVVHEEFGILGGLHTVHATTATQKTVDGPS
MKDMRGGGGASQNIIFSSTGAAKAVGKVLPELNGKLTGMAFFRVPTSNVSVDLTCRLE
KGASYEDVKAAIKHASEGPLKGILGYTDEDVSNDFVGDSRSSIFDANAGIGLSKSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Is a member of the PF|00044 glyceraldehyde 3-phosphate dehydrogenase family. ESTs gb|T43985, gb|N38667, gb|N65037, gb|AA713069 and gb|AI099548 come from this gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPDIILYTILIQGLSKAGKIEDALKLLSSMPSKGISPDTYCYNAVIKALCGRGLLEEG
RSLOLEMSETESF PDACTHTILICSWCRNGLVREAEELFTEIEKSGCSPSVATFNALI
DGLCKSGELKEARLLLKMEVGRPASLIFLRLSHSGNRSFOTHVESGSILKAYBDLAHF
ADTGSSPDIVSYNVLINGFCRAGDIDGALKLLNVLQLKGLSPDSVTYNTLINGLHRVG
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KMFDDMTGRGISPNRVTYTILISGLCQRGSADDARKLFYEMQTSGNYPDSVAHNALLD
GFCKLGRMVBAFELLALFEKDGFVLGLRGYSSLIDGLFRARRYTQAFELYANMLKKNI
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                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24955. .25185,25275. .25613,26424. .26525)
/gene="TRK14.6"
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KKILVTPPSCVKLIHGLCKREQLDAAIEVFLYTLDNNFKLMPRVCNYLLSSLLESTEK
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KPIEPALEPLVPFLSKNIITSVIKDEVNRQLGFRFFIWASRRERLRSRESFGLVIDML
SEDNGCDLYWQTLEELKSGGVSVDSYCFCVLISAYAKMGMAEKAVESFGRMKEFDCRP
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/protein_id="AAD30222.1"
/db_xref="GI:4835755"
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15312. .17654
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/gene="T8K14.4"
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                                                      clone CTD-2040H20,
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AP003046
           Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp/, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Mar 28, 2001 this sequence version replaced gi:11862976.
Genes were predicted from the integrated results of the following:
                                                                                                          Submitted (13-DEC-2000) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kanno
 GENSCAN1.0,
                                                                                                                                                                                                                                   clone: P0445D12
                                                                                                                                                                                                                                                Oryza sativa nipponbare(GA3) genomic
                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                               Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (cultivar:Nipponbare) DNA, clone:P0445D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Sep 9, 2000 this sequence version replaced gi:9256045. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 117018)
                                                                                                                                                        Direct Submission
                                                                                                                                                                       Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                           Published Only in DataBase (2000) In press
                                                                                                                                                                                                                                                                    Sasaki,T., Matsumoto,T.
                                                                                                                                                                                                                                                                                                                                                                                                                        AP003046.2 GI:13486797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             www.jqi.doe.qov
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/db_xref="taxon:9606"
/chromosome="5"
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7a genomic DNA, chromosome 1,
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BLASTN2.0, BLASTX2.0 as well as SplicePredictor
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                                                                                                                                                                                                                                                                                                          Oryza.
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The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0445D12 clone has an overlap with P0684C01 (DDBJ: AP002487) clone at the position 1 to 17,951 of 5' end. The sequence of this clone starts at the position 60650 of P0684C01. Detailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          corresponding DDBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (October 1998 version).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein homologies of the coding regions were searched against NonRedundant Protein database with BLASTP2.0. ESTs represent
RDGPTNKVRARMSVASAIIFGSVFWRMGKTQTSIQDRMGLLQVTAINTAMAALTKTVG
VFPKERAIVDRERAKGSYALGPYLSSKLLAEIPIGAAFPLIFGSILYPMSKLHPTFSR
FAKFCGIVTVESFAASAMGLTVGAMAPTTEAAMALGPSLMTVFIVFGGYYVNPDNTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(17738 ..17923,18232 ..18316,18417
18768 ..18988,19165 ..19296,19872 ..20148,20541 ...
21433 ...21565,21895 ...22045,22138 ...22328,22821 ...
/gene="p0445D12.3"
complement(join(17738 ...17923,18232 ...18316,18417
                                                                                                                                                                     ELQLRRTLTPERKESYVNDLLFRLGLVNCADSIVGDAKVRGISGGEKKRLSLACELIA
SPSIIFADEPTTGLDAFQAEKVMETLRQLAEDGHTVICSIHQPRGSVYGKFDDIVLLS
                                                                                                                                                                                                                                                                  /translation="MEVRGLGQLLAALAAALFVRAVAGPGPALLPPADDEDSDADPEA
GGEGGGVPPVTIRWARITCALKNKRGDVARFLLSNASGEAKSGRLLALMGPSGSGKTT
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VDSSMAVLRRRMREARMAENNYEAPAGWSAWEKRYYPAYVSDVSAAVGALQLLLMGTR
PSVAIAAAALLFAGVPVSAVAAVHHLAQLAAESAVLLQHHVVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(3938. .4150,5347.
/gene="P0445D12.1"
                                                                                                    EGEVIYMGPAKEEPLLYFASLGYHCPDHVNPAEFLADLISVDYSSAESVQSSRKRIEN
LIEEFSNKVAITESNSSLTNPEGSEFSPKLIQKSTTKHRRGWWRQFRLLFKRAWMQAF
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21433. .21565,21895. .22045,22138. .22328,22821. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(16002..16439)
/gene="P0445D12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0445D12.2"
complement/177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKLTWSESKQSRSAIIIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAB40030.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(3938. .4150,5347.
/gene="P0445D12.1"
                                                                                                                                                                                                                                          LLNVLAGQLTASPSLHLSGFLYINGRPISEGGYKIAYVRQEDLFFSQLTVRETLSLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="contains ESTs AU093168(C0321),D15235(C0321)
                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="P0445D12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:13486799"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="P0445D12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4530"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .14095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .5445,6717.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .18316,18417.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .6767))
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.23036))
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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRERSSPAALPGHLAAGHSWPVAEIAYGKPKKLAVPPPAHVLVGEADRAVFLVSSCAV
GAGAAVCVVCVRANGGGDNAAAVARYKCKLWVEVPSINDNMAMMTSMVRSSDLAGGFP
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complement(join(38187. .38413,38479. .38682,39059. .39788)/
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RAARCGRPARDAGAHSCRSGGRCDGGATTGYATRRRQPATPHRYASDAMAPSCRSDGP
                                                                                                                                                                                       complement(join(44730. .44939,45033.
/gene="p0445D12.8"
                                                                                                                                                                                                                                                                                    DPGCGFRGSPAALLGHFATDHPWSVTQISYAKPCRLAVPLPRRCHVLVGEDDRAMFLV
VSPSPCGVGVGAAVCVACVRANGDDAAAAQYKCKLWVEVPTNSDNMVMMTSKVRSSDL
SGGFPAAEQGMFLVVPPELLHEVSGETPILSIRIDRAAPAIAKPTTPRARSLRRLQ"
                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB40036.1"
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GQLCRRAAAYAHCAELDAIVGAAKVACAHAPYGCDSYVVYGAAAEHQRACPCAPCSCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGAGDSKLGGGARREERDGEGEQENEKEGELGSASAHAHARATHGRDEGEEG join(42735. .42995,43154. .43891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MGRPAREGGPRHAREGRRGGASGPGSPRVVPSGTRLSVARFTVR
REHAARAR IWGRDAVHARGSRCCGCGGTRSLMAHGGPRARAGGRGAADRGRLDPVLA
ELAPTWRLRCCHTGRREVEDCAGQNGRRTAAYNGGANHGDTGGSGHTGWLHETR&DDF
TARIRRELDGGGLRRRQPSAREGGNGDGATGGRFGRARASTRLRESVSSVRLDGDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(38187. .38413,38479. .38682,39059./gene="P0445D12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="BAB40034.1"
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/translation="MVEQNKRARANGEVKQEQQQEEEEEVEEGEVSQEETQRTGAFPL
VTMAAMEQTEEETQIDVRIAVALLHCHACLQPLKEPVEKCDBAHIVCSGCRCGHHGQL
CGGAAVYSHCAELDAIVATAKVPCAHAPYGCSSYVVYAGVADHQRACPCAPCSCPEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSRAAPAVRAFGNVDVVGRPTAGTPMGSSGLAATLRAAAALLRLDSEWDWFVTLNAAD
YPLVTQDDLIHVFSSVPRHLNFIDHTSDIGWKETQRVQPIIVDAGIYLAGRNQFFQAT
EKRDTPDGFKFFTGSPWVILNRRFIEYCIFGWENLPRTLLMYFTNVMLPQEGYFHSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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/VRRGAAAPPSFAYVLSGGRGEERKLLFLLLAYVHPRNNYLLHLSADAPSSERVELAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFRWIPKVSLIRWAFQGLCINEFKGLQFEQQHSYDIQTGEQALERFSLGGIRIADTLV AQGRILMFWYWLTYLLLKKNRPKYQQLLPPSEEDQNKQQVKEVK" join(25341. .25842,28143. .28218,28300. .28415,28495. .2900
                                                                                                                                                                                                                                                             complement(join(44730. .44939,45033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(42735. .42995,43154. .43891)
/gene="P0445D12.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRLASCHFGKRRKEREGDEAVGGGALPPILGSMRGGRQALTAAATGRSATTARARAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JUIN(33714. .33962,34268.
/gene="P0445D12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNSDFRNSTVNSDMRYMEWDDPPQMEPHFLNTTHYDEIVESGVPFARKFRENEPLLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown protein"
                                                                                             /protein_id="BAB40037.1"
/db_xref="GI:13486805"
                                                                                                                                                                                                                                         /gene="P0445D12.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt REAGDVWALPSTGGDGGEHTASGGNGRSKSKLALGGHGQNGDREDDAGGEKKEERKGE}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB40035.1"
/db_xref="GI:13486803"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(33714. .33962,34268.
/gene="P0445D12.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="P0445D12
join(25341. .25
                                                                                                                                                                   'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="P0445D12.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDERVLHRWRHRPVPGAWCTGRKRWFNDPCSQWSNVNIVRPGPQAEKFRKHMNQIIEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .25842,28143.
5D12.4"
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                                                                                                                                                                                                                   .45272))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 22
AL161454/c
                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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80 tcacatgtaaggtgatac 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(50655. .51095)
/note="3' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(48421. .48594,48714. .48845))
/gene="p0445D12.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mQHGEQSGAKKAAAWVVSPNGQVKREMAVEAARGEGAAAAAGAG
EEEEEEVQAGGMIAAAVGDGFEGVEISVRIDLAVLHCPLCLLPLKPPTYQCAAGHLACS
SCHGDVPGKKCHTCGGGGGGGVYARCPGLDTFLRAAKILCPNDLFGCRSYVAYHDVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (13-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(51250. .54737)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mGEGRWPAATEAVGAKEVAAGVGDLVAAPNMARRCPSADEDDDA
PGPADFLLRNEVGNLTEITDKKRLPTKRSEKTPYHFRYHFRKRLPFPFPFPTTTDTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(48421. .48594,48714.
/gene="p0445D12.10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAB40039.1"
/db_xref="GI:13486807"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HQRACPHAPCSCSEPRCDFLGSPPMLLAHLVADHSWPVSKVPYGEVLTIHVPESERRH
LVVAGAAGGDDERVFVLSVGALGVARAVSVACVRANAAAGPRYRCKLWAHAPGGGAAD
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/db_xref="GI:13486806"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(46910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="P0445D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144536 bp DNA rn1 2-- 9, complete sequence from clone RP11-72B4 on chromosome 9, complete
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5D12.9"
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;D12.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone RP11-72B4 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-72B4 is at 1 in this sequence. true left end of clone RP11-18014 is at 142537 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapp Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/HGP/Chr9
RPI1-72B4 is from the library RPCI-11.1 constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             true right end of clone RP11-346B7
                                                             note="L1ME2 repeat: matches 5913. .6162 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                      note="MER5A repeat:
                                                                                                                                                                 note="L1PA3 repeat: matches 5359. .6142 of consensus"
4647. .15016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .one_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      te="MLT1D repeat: matches 1. .184 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       te="MER47 repeat: matches 2242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e="MER47 repeat: matches 2265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="18 copies 2 mer ac 97% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .8304
:e="L1MC4 repeat: matches 7813. .7952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e-"MIR repeat: matches 15.
                   e="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   e="L1M4 repeat: matches 5160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e="THE1B repeat: matches 1. .364 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="AluSx repeat: matches 1. .302 of consensus"
                                                                                                                                                e-"THE1C
                                                                                                                                                                                                                                                                                                                                            >="L1M4 repeat: matches 3504.
1. .10777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="MIR repeat: matches 103. .146 of
                                                                                                                                                                                                                                                                                                                                                                                        p="MLT1C repeat: matches 20.
1. .10623
                                                                                                                                                                                                                                                                                                                    -"AluJb repeat:
                                                                                                                                                                                                                               -"L1PA3 repeat:
                                                                                                                                                                                                                                                                        "MLT1D repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .9430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "L2 repeat: matches 1852. .3419
                                                                                                                            .15290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .4149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 5993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alu repeat: matches 233. .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIMC4 repeat: matches 6822. .7608 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1M4 repeat: matches 5276. .5321 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 further details see
                                                                                                                                              repeat:
                     matches 15.
                                                                                                                                                                                                                                 matches 4256. .5387 of consensus"
                                                                                                                                                                                                                                                                            matches 1. .417 of consensus*
                                                                                                      matches 9. .178 of
                                                                                                                                              matches 1. .371 of
                                                                                                                                                                                                                                                                                                                        matches
                                                                                                                                                                                                                                                                                                                        84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is at 81734 in this
                   .262 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2745 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                       .466 of consensus"
                                                                                                                                                                                                                                                                                                                        .206 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                .5276 of consensus"
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                                                                                                      consensus"
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/note="L1MC2 repeat: matches 5193. .6224 of consensus"
30430. .50717
                                                                                                                                                                                                                                                                                                                                                                     note="L1MD1 repeat: matches 5374. .6224 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1MEc repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Aluy repeat: matches 1. .296 of consensus"
18257. .18527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restriction
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restriction digest data."
                                                                                                                                                                                                                                                                                       'note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                               'note="MIR repeat: matches 177. .256 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                               'note="L1MEc repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="MER11C repeat: matches 1. .1071 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="AluSc repeat: matches 1.
                                                                                                                                                                                                                                               note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1 repeat: matches 3596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Alusx repeat: matches 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1M4c repeat: matches 1489. .1687 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="L1MB3 repeat: matches 5893. .6175 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 te="AluSx repeat: matches 1.
e="AluSc repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e="LlM4 repeat: matches 2773. .2896 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e="L1MD repeat: matches 21. .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e="TIGGER1 repeat: matches 1. .1792 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e="AluSg1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ="L1M4 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ="MER5A repeat: matches 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "L1 repeat: matches 1910. .2104 of consensus" .21472
                                                                                                                                                                                                                              .38960
                                                                                                                                                                                                                                                                                                                                                                                                                                      .34100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .28088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .19616
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                                                                                                      .40792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MD repeat: matches 179.
2557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat: matches 2138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       copies 2 mer tt 60% conserved
                                                                             repeat:
                                                                                                                     repeat:
                                                                                                                                                                                                     repeat: matches 4487. .4585 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 2510. .2574 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 1. .293 of consensus"
                                                                                                                                                               repeat: matches 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat:
                                                                                                                                                                                                                                               matches 22. .177 of consensus"
                                                                               matches
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                                                                                                                                                                                                                                                                                                                                                                                                               matches 2406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      matches 1761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matches 5173.
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                                                                               883.
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                                                                                        Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 6% of reads Ch
Dye-terminator Big Dye; 93% of reads
Consensus quality: 143907 bases at least Q40
Consensus quality: 144683 bases at least Q30
Consensus quality: 145697 bases at least Q20
Insert size: 145671; sum-of-contigs
Insert size: 155726; 1.2% error; agarose-fp
Quality coverage: 7.35x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes clonerequest@sanger.ac.uk
On Jul 4, 2001 this sequence version replaced gi:14587003.
                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                       Center project name: bA63N8
----- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome
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NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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58890. .59017
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UENCING IN
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* 24805 24904: gap of 100 bp

* 24905 35138: contig of 10234 bp in length

* 35139 3528: gap of 100 bp

* 35239 54888: contig of 19650 bp in length

54889 54988: gap of 100 bp

54989 69175: contig of 14187 bp in length

69176 69275: gap of 100 bp

69276 84233: contig of 14958 bp in length

84334 99092: contig of 14958 bp in length

84334 99092: contig of 14759 bp in length

99193 102346: contig of 3152

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102447 116814: contig of 14368 k
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/db_xref="taxon:9606"
/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 139048 bases at least 040
Consensus quality: 147965 bases at least 030
Consensus quality: 147145 bases at least 020
Estimated insert size: 150000; pulse field gel estimation
Estimated insert size: 148148; sum-of-contigs estimation
Quality coverage: 5.82 in 020 bases; pulse field gel estimation
Quality coverage: 5.89 in 020 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-APR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:7712076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 148498)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: CITB-H1_2124P14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center Project Name: 675539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 148498)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing of Human Chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, 8 ordered pieces.
                                                                                                                                                                                                                                                  by the finished sequence as soon as it is available and the accession number will be preserved.

1 61862: contig of 61862 bp in length 61863 61962: gap of unknown length 61963 68022: contig of 6060 bp in length 68023 68022: contig of 6060 bp in length 68023 68122: gap of unknown length 68123 80136: contig of 12014 bp in length 80137 80236: gap of unknown length 80237 83311: contig of 3075 bp in length 83311: contig of 3075 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                    provided by the submittor. This sequence will be replaced
                                                                                                          92461
120403
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88934
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                                                                                                                                                                                                                                           61963
68023
68123
68137
80137
80237
                                                                                                                                                       92361
/db_xref="taxon:9606"
                 /organism="Homo sapiens"
                                                                Location/Qualifiers
                                                                                  92460: gap of unknown length
120402: contig of 27942 bp in
120502: gap of unknown length
148498: contig of 27996 bp in
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                                                                                                                                                                  83411: gap of unknown length
88833: contig of 5422 bp in length
88933: gap of unknown length
92360: contig of 3427 bp in length
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5 clone CTD-2124P14, WORKING DRAFT
                                                                                  in length
                                                                                                                          in length
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AL357252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burton,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases
                                                                                                      51406 51505:
                                                                                                                                            36987 37086:
                                                                                                                                                                      21852 21951:
21952 3698
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Db 32644 CAACCCTGATGACCTAAT 32661
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 150971 bases at least Q40
Consensus quality: 151464 bases at least Q30
Consensus quality: 151889 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                               * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 152505; sum-of-contigs
Insert size: 157709; 4.7% error; agarose-fp
Quality coverage: 7.06x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coverage: 6.89x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: bA35C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 7, 2001 this sequence version replaced gi:12227371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-MAY-2001) Sanger Centre, Hinxton, Cambridgesh: CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clonerequests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL357252.8 GI:13990058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROGRESS ***, 10 unordered pieces
                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="CalTech human B# 44488 a 30209 c 29485 g 43610 t
                                               54731 54830: gap of 100 bp
54831 75701: contig of 20871 bp in length
75702 75801: gap of 100 bp
75802 85440: contig of 9639 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 to 153405)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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116412: cont
                                                                                                                                                                505: gap of 100 bp
54730: contig of 3225 bp in length
                                                                                                                                                                                                                   51: gap of 100 bp

100 bp in length

100 bp in length

100 bp in length

100 bp in length
                                                                                                                                                                                                                                                                                                                              21851: contig of 21851 bp in length
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  p of 100 bp
contig of 30872 bp in length
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UENCING IN
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REFERENCE
AUTHORS
TITLE
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ORIGIN
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                                                                                                                                                                                                    RESULT
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Best Local
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                                                                                                                                                                                                                                              AATTTATTCCACACAACA 37948
                                                                                                              Homo sapiens chromosome 4 clone RP11-394N5 map 4, WORKING DRAFT SEQUENCE, 28 unordered pieces.
AC023537.2 GI:7229813
             Birren, B., Linton, L.,
                                                                                                   HTG;
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                       Homo sapiens
                                                                                                                                                                        AC023537
                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                         33074
                            (bases 1 to 156795)
sapiens chromosome 4, clone
                                                                                                HTGS_PHASE1;
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141141 145417
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116513 14104(
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85541. .1
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fragment_chain:2"
145518. .153405
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fragment_chain:2"
116513. .141040
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fragment_chain:2"
    40678 c    42451 g    36301 t
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fragment_chain:2"
141141. .145417
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/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment:01594
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment:02618
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment:02549
fragment_chain:1"
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fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment:02366
fragment_chain:1"
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/clone_lib="RPCI-11.1"
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ap of 100 bp
contig of 24528 bp in length
ap of 100 bp
                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                 Score 18;
Pred. No.
              Nusbaum, C.
                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                 DB
15;
 RP11-394N5
              and Lander, E
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                                                                                                                                                                                                                                                                                                                               Length 153405;
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JOURNAL
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J., Morman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wal, Y., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 12, 2000 this sequence version replaced gi:6978216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage, Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DeArellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                         Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 137441 bases at least Q40
Consensus quality: 147789 bases at least Q30
Consensus quality: 151521 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 154095; sum-of-contigs
Quality coverage: 3.2 in Q20 bases; agarose-fp
Quality coverage: 3.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: 394_N_5
------ Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L5543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Castle, A.,
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as soon as it be preserved. 3058 5036: contig of 2033 bp in length 5097 5196: gap of 100 bp 7059: contig of 1863 bp in length 7060 7159: gap of 100 bp 100 b 2957: contig of 1446 bp 2958 3057: gap of 100 bp 3058 5096: contin 1411: contig of 1411 bp in length 1: gap of 100 bp 2957: contig of 1446 bp in length

soon as it is available and the

accession number will

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81246 88655:

88656 88755: ga

88756 97086: ga

97087 97187: 107056: ga

107057 119495:
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119495: contig of 12439 bp in
119496 119595: gap of 100 bp
119596 134366: contig of 100 bp
134367
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134367 134466: gap of 100 bp
134467 156795: contig of 22329 bp in length
Location/Qualifiers
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18336 18435: gan
18436
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128 24224: contig of 2097 bp in 16
128 24224: contig of 2097 bp in 16
125 24324: gap of 100 bp
170 27069: gap of 100 bp
170 30436: contig of 3367 bp in 16
137 30536: gap of 100 bp
137 30536: gap of 4264 bp in 16
137 34800: contig of 4264 bp in 16
/note="assembly_fragment"
24325. .26969
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11861. .13457
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/db_xref="taxon:9606"
                                                                                                                                 note="assembly_fragment"
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/clone_lib="RPCI-11 Human Male
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18435: contig of 2676 bp
18435: gap of 100 bp
20122: contig of 1687 bp of
20222: gap of 100
20227: contig of 100
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BASE COUNT
ORIGIN
 Matches
            Query Match
Best Local
                                                                                                        misc_feature
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 18;
             Similarity
                                                                             47744 a 27616 c 27899 g
 Conservative
                                                                                                        vector_side:left"
134467. .156795
                                                                                                                                                                                    /note="assembly_fragment"
97187. .106956
/note="assembly_fragment"
107057. .119495
                                                                                                                                                                                                                                         /note="assembly_fragment"
88756. .97086
                                                                             /note="assembly_fragment"
27616 c 27899 g 50833 t
                                                                                                                                  clone_end:SP6
                                                                                                                                                                                                                                                                  /note="assembly_fragment"
81246. .88655
                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
57333. .64959
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27070. .30436
                                                                                                                                            /note="assembly_fragment
                                                                                                                                                                        /note="assembly_fragment"
                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
72969. .81145
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            14.6%;
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                                                                                                                                                                                                                                                                                                                          .72868
0;
            Score 18;
Pred. No.
 Mismatches
            DB
15;
                         2;
0,
                                                                             2703 others
                         Length 156795;
Indels
0;
Gaps
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0

REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS RESULT 27 AC024315/c LOCUS DEFINITION JOURNAI ORGANISM 2 (bases 1 to 165858)

2 (bases 1 to 165858)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Boukhqalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Charellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Fernestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Graham, L., Graham, L., Graham, C., Grant, G., Hagos, B., Heaford, A., Horton, L., 1 (bases 1 to 165858)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-26N3
Unpublished Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens AC024315.3 GI:8072573 HTG; HTGS\_PHASE1; HTGS\_DRAFT pieces Homo AC024315 sapiens 165858 b bp DNA HTG RP11-26N3, WORKING DRAFT 26-MAY-2000 SEQUENCE, 14 unorc unordered

JOURNAL

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Klein, J., Landers, T., Largocque, K., Lenoczky, J., Leville, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McDarthy, A., McMarthy, A., Maylor, J., Mihoya, T., Mihoya, T., Minanda, C., Mlenga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and
27435: contig of 8582 bp in length
27436 41698: contig of 100 bp
41799 54767: contig of 12969 bp in length
54768 70975: gap of 100 bp
70876 70975: gap of 100 bp
70876 87982: contig of 17007 bp in length
70876 80812: contig of 100 bp
70878 70975: gap of 100 bp
70978 87983 80082: gap of 100 bp
70978 87983 80082: gap of 100 bp
70978 10013: contig of 12007
7014 10213: gap of
7014 10213: gap of
7014 133760: contig of 2207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Howland, J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 4.6 in Q20 bases; agarose-fp Quality coverage: 4.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consensus quality: 154942 bases at least Q40 Consensus quality: 159890 bases at least Q30 Consensus quality: 162505 bases at least Q30 Insert size: 164000; agarose-fp Insert size: 164558; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L4668
Center clone name: 26_N_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 1274: contig of 1274 bp in length
1275 1374: gap of 100 bp
1375 2528: contig of 1154 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2528: contig of 1154 bp in length
2628: gap of 100 bp
4506: contig of 100 bp
4606:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6547: gap of 100 bp
11790: contig of 5243
11890: gap of 100 bp
18653: contig of 6763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4606: gap of
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contig of 1841 bp in length
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REFERENCE
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                                                                                                                                                                                                           KEYWORDS
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                                                                                                                                                                                                                                                                                                                 AC009776
                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                 Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                         AUTHORS
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                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; i
1 (bases 1 to 183496)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R.,
Alisbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., i
                                                                                                                                                                                                                                                           Homo sapiens chromosome 12 clone RP11-333I15, WORKING DRAFT SEQUENCE, 22 unordered pieces.
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                             AC009776.8 GI:10445255
                                                                                                                                                                                                                                                                                                   AC009776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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133861 165858: contig of 31998 bp in length.
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34483 c 34023 g 47184 t
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP11-26N3"
                                                                                                                                                                                                                                                                                                 183496 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.6%; Un
100.0%; Pr
0;
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3. .110113
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                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.
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15;
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                                                                                     Barbaria, J.,
                                                                                                                                         Homo.
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                                                                                                       Allen, C.,
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Foster, P., Frantz, P., Gabisi, Ferrayuv, F., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunrathe, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Harr, M., Havlak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Matting, P., Martin, R., Martindle, A., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Moyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oyuh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oyuh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oyuh, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Shooshtari, N., Stone, H., Shooshtari, N., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tang, S., Watch, N., Watliamson, A., Washington, C., Watliams, G., Williamson, A., Washington, C., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 2, 2000 this sequence version replaced gi:10047636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
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                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                            (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 22 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length
                                                                                                                                    as soon as it is available and the be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-primer Bodipy: 61% of reads chemistry: Dye-terminator Big Dye: 39% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 165672 bases at least Q40 Consensus quality: 174319 bases at least Q30 Consensus quality: 174319 bases at least Q30 Consensus quality: 178820 bases at least Q20 Estimated insert size: 176791; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: HMJH
Center clone name: RP11-333115
Center clone name: RP11-333115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 3.8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
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29141
29040: contig of 29040 bp in length 29140: gap of unknown length 48361: contig of 19221 bp in length
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REFERENCE AUTHORS TITLE

JOURNAL

TITLE JOURNAL

COMMENT

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KEYWORDS
SOURCE
ORGANISM
                                                                                                                AC068581
        REFERENCE
                                                                                              DEFINITION
                                                                                                                                                      Db 180935
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19063)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                     Homo sapiens
                                                       AC068581.2 GI:10280770
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                           AC068581
                                                                                            AC068581 190663 bp DNA HTG 23-SEP-2000 HOMO Sapiens chromosome 4 clone RP11-598012 map 4, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Kalein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Palani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 23, 2000 this sequence version replaced gi:7705127. All repeats were identified mains passet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tresfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N. Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
              4554 4653; contig of 4553 bp in length
4554 4653; gap of 100 bp
4654 5713; contig of 1060 bp in length
5714 5813; gap of 100 bp
5814 9313; contig of 3500 bp in length
9314 9413; gap of 100 bp
9414 12245; contig of 2832 bp in length
12246 12345; gap of 100 bp
12346 15186; contig of 2841 bp in length
15187 15186; contig of 3876 bp in length
15187 15162; contig of 3876 bp in length
19163 19262; gap of 100 bp
19163 19262; gap of 100 bp
19263 23897; contig of 4635 bp in length
19163 19262; gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
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L, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 4.0 in Q20 bases; agarose-fp Quality coverage: 4.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: 598_0_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 194000; agarose-fp
Insert size: 188563; sum-of-contigs
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Grant,G., Hagos,B., Heaford,A., Horton,L.,
Grant,G., Johnson,R., Jones,C., Kann,L., Kara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collins, S.,
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111078 125542: cont
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27486 27585: gap of 100 bp
27586 31745: contig of 4160 bp in length
31746 31845: gap of 100 bp
31846 36461: contig of 4616 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50664 50763:
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16562 42979: contig of 6418 bp in length
2980 43079: gap of 100 bp
3080 50663: contig of 7584 bp in length
3080 50663: contig of 7584 bp in length
3064 50763: gap of 100 bp
30764 58952: contig of 8189 bp in length
8953 59052: gap of 100 bp
30753 59052: gap of 100 bp
30776 67875: contig of 8723 bp in length
37776 67875: gap of 100 bp
3789: gap of 100 bp
                                                                                /note="assembly_fragment"
77890. .86920
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67876. .77789
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59053. .67775
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50764. .58952
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190663: contig of 13782 )
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141160: contig of 15518 l
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110977: contig of 23957 bp
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ORGANISM
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                                                Consensus quality: 177736 bases at least Q40
Consensus quality: 184740 bases at least Q30
Consensus quality: 186701 bases at least Q20
Estimated insert size: 192000; agarose-fp estimation
Estimated insert size: 192000; agarose-fp estimation
Cuality coverage: 8.68 in Q20 bases; agarose-fp estimation
Quality coverage: 8.74 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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18; Conservative
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Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 192430)
DOE Joint Genome Institute.
Sequencing of Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Summary Statistics
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Center Project Name: 1880143
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DOE Joint Genome Institute.
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154918. .176781
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176882. .190663
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141261. .154817
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125643. .141160
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100.0%; Pred. No. 15
:ive 0; Mismatches
1123: contig of 1123
1223: gap of unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RP23-373B15, WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
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   bp in length
length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGGCTGCACTGACTGG 134532
                                                Submitted (03-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 7, 2001 this sequence version replaced gi:12329367.
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 198605)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome 1 clone RP11-506024, 
PROGRESS ***, 8 unordered pieces. 
AL357568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
18; Conserv
                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                          Burton, J
                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   AL357568.11 GI:13990061
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL357568
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4938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-373B15"
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                           Genome Center
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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g of 9610 bp in 10
f unknown length
g of 12325 bp in
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of 8497
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of 2360
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of 6136
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of 3431
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of 1739
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of 39878 bp in
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SEQUENCING IN 03-MAY-2001 23" others

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 197905; sum-of-contigs
Insert size: 138913; 37.8% error; agarose-fp
Quality coverage: 7.56x in Q20 bases; sum-of-contigs Quality
coverage: 10.97x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129888; contig of 25724 bp in length 129888 gap of 100 bp 129988 contin of 100 bp 129989 139533; contin of 100 bp 129989 139534 17acco
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25046 25145: gap of 100 bp

25146 33473: contig of 8328 bp in length

33474 3373: gap of 100 bp

33574 79364: contig of 45791 bp in length

79365 79464: gap of 100 bp

79465 104064: contig of 24600 bp in length
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                    //note="assembly_fragment:02854.0"
157595. 1198605
/note="assembly_fragment:03653"
/note="assembly_fragment:03653"
40525 c 41243 g 58791 t 70
                                                                                                                                                                                                                                                                                                                                                                 33574
                                                                                                                    /note="assembly_fragment:00526.1"
139634. .157494
                                                                                                                                                                 /note="assembly_fragment:00526.0"
129989. .139533
                                                                                                                                                                                                                    104165
                                                                                                                                                                                                                                     /note="assembly_fragment:01381
fragment_chain:1"
                                                                                                                                                                                                                                                                                                            /note="assembly_fragment:02873
fragment_chain:1"
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment:02045
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP11-506024"
/clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29988: gap of 100 bp
139533: contig of 9545 bp
39633: gap of 100 bp
157494: contig of 17861 b
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198605: cont
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                      701 others
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Query Match Best Local Similarity

14.6%; 100.0%;

Score 18; Pred. No.

DB 2; 15;

Length 198605;

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Chauer, S., Severy, P., Chaman, C., Chauer, S., Severy, P., Spencer, B., Chauer, S., Severy, P., Chauer, S., Severy, P., Rothman, D., Chauer, S., Severy, P., Spencer, B., Chauer, S., Severy, P., Spencer, B., Chauer, S., Severy, P., Chaman, C., Chauer, S., Severy, P., Chauer, S., Severy, P., Chauer, S., Severy, P., Chaman, C., Chauer, S., Severy, P., Chauer, S., Severy, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-MAR-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 25, 2001 this sequence version replaced gi:8077096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996–1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkly,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stange-Thomann, N. Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, I., Veng, G., Zainoun, J., Zimmer, A. and Zody, M.
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Galagan,J., Gardyna,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren,B., Linton,L., Nusbaum,C. and Lander,E. mus musculus chromosome 10, clone RP23-129023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC025501.4 GI:14547868
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                                                                                                           Sequencing vector: Plasmid; n/a; 56% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 213014 bases at least 040 Consensus quality: 214764 bases at least 030 Consensus quality: 21528 bases at least 020 Insert size: 210000; agarose-fp Insert size: 216373; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 10
Quality coverage: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; M77815; 44% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead
Center code: WIBR
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lus chromosome 10 clone RP23-129023 map 10, WORKING DRAFT 18 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (09-MAR-2000) Whitehead Institute/MIT Center for Genome 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- Genome Center
'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                  10.2 in Q20 bases; agarose-fp 9.9 in Q20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133851 151236: contig of 17386 bp in
151237 151336: gap of 100 bp
151337 174475: contig of 23139 bp in
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28341. .30420
                                                                                                                                   /note="assembly_fragment"
32232. .34170
                                                                                                                                                                                                                                             27060.
/note="assembly_fragment"
13466. .46874
                                /note="assembly_fragment"
10450. .43365
                                                                   /note="assembly_fragment"
36817. .40349
                                                                                                                  /note="assembly_fragment"
                                                                                                                                                                                                                                                                               24630
                                                                                                                                                                                                                                                                                                                         vector_side:left"
                                                                                                                                                                                                                                                                                                                                                 clone_end:SP6
                                                                                                                                                                                     note="assembly_fragment"
                                                                                                                                                                                                                                                       /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                         note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 'chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location,
                                                                                                                                                                                                                                                                                                                                                             note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46974: contig of 3409 bp
46974: gap of 100 bp
51691: contig of 4717 bp
51791: gap of 100 bp
118666: contig of 66076:
                                                                                                                                                                                                                                                                                                                                                                                                                 lone="RP23-129023"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33850: gap of 100 bp 151236: contig of 17386 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30420: contig of 2080 bp

30420: contig of 2080 bp

0520: gap of 100 bp

32131: contig of 1611 bp

2231: dan of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7059: gap of 100 bp 28240: contig of 1181 bp 18340: gap of 100 bp 30420: contig of 2080 bp 0520: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218073: contig of 9276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4575: gap of 100 bp
208697: contig of 34122 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36716: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231: gap of 100 bp
34170: contig of 1939 bp
270: gap of 100 bp
36716: contig of 2446 bp
36716: contig of 353 bp
40349: contig of 353 bp
443: gap of 100 bp
43365: contig of 2916 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23321: contig of 23321 bp in length 421: gap of 100 bp 24529: contig of 1108 bp in length 529: gap of 100 bp 529: gap of 2330 bp in length
                                                                                                                                                                                                                                           .28240
                                                                                                                                                                                                                                                                             . 26959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Qualifiers
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AC079583/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAGTTTCACATGTAAGG 133452
                                   Consensus quality: 209212 bases at least Q40
Consensus quality: 215597 bases at least Q30
Consensus quality: 215597 bases at least Q30
Consensus quality: 216943 bases at least Q20
Estimated insert size: 212000; agarose-fp estimation
Estimated insert size: 224260; sum-of-contigs estimation
Quality coverage: 10.49 in Q20 bases; agarose-fp estimation
Quality coverage: 9.92 in Q20 bases; sum-of-contigs estimation
Quality coverage: 9.92 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pleces.
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                            Summary Statistics
                                                                                                                                                                                                                                                                                                    Center clone name: RPCI-23_9G1
                                                                                                                                                                                                                                                                                                                          Project Information Center Project Name: 1740473
                                                                                                                                                                                                                                                                                                                                                                                                             Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 226060)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 226060)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jnpublished
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown
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a 47778 c 47469 g
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208798. .218073
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174576. .208697
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46975. .51691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226060 bp DNA HTG 02-SEP-2000 us clone RP23-9G1, WORKING DRAFT SEQUENCE, 19 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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REFERENCE
AUTHORS
                                                   SOURCE
ORGANISM
                                                                                                                          RESULT 3
AX044029
                                                                                                     DEFINITION
                                                                                                                                                                   Db 174925 GAGGGCTGCACTGACTGG 174908
                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                        KEYWORDS
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                                                                                             ACCESSION
                                                                                                                  Locus
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Best Local 9
                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                              56 gagggctgcactgactgg 73
                                                                                                                                     34
                                                                                             Sequence
AX044029
Pizza,M., Hickey,E., Peterson,J.,
Masignani,V., Galeotti,C., Mora,M
                                                                                                                                                                                                           . Similarity
18; Conserv
                                                 Neisseria meningitidis.
Neisseria meningitidis
                                                                                  AX044029.1 GI:11342913
                                                                                                                AX044029
                                Neisseria.
                                          Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                       56590
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                    (bases 1 to 349980)
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5395
5495
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108 from
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                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-9G1"
                                                                                                                                                                                                                                                                                                                       1. .226060
                                                                                                                                                                                                                                                                                                                                   Location
                                                                                                                                                                                                                                                                                                                                                              97871: gap of unknown length
116093: contig of 18222 bp in 1
116193: gap of unknown length
141239: contig of 25046 bp in 1
141339: gap of unknown length
177145: contig of 35806 bp in 1
                                                                                                                                                                                                                   14.6%;
                                                                                                                                                                                                                                                                                                                                           177245: gap of unknown l
226060: contig of 48815
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193: gap of unknown length

396: contig of 12303 bp in la

396: gap of unknown length

1973: contig of 10377 bp in la

173: gap of unknown length

171: contig of 20598 bp in la

171: gap of unknown length

1871: gap of unknown length

1871: gap of unknown length
                                                                                                     ) bp p
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                                         beta subdivision; Neisseriaceae;
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 Mora,M.,
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of 4437
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Jof 3833
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f of 1030
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of 9146 bp in length
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Venter, J.C.,
Scarselli, M.,
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AUTHORS
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01-NOV-2000
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l Similarity 100
17; Conservative
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Drosophila melanogaster

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 518)

Davies, R.W., Kalser, K.U. and Yang, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
AX094499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Essential genes and assays relating thereto Patent: WO 0118547-A 623 15-MAR-2001; THE UNIVERSITY OF GLASGOW (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AX094499.1
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/db_xref="taxon:7227"
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/db_xref="taxon:487"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Botany, University Blvd., Vanc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished.
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Eukaryota; Alveolata;
Heterocapsa.
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                    The
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                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                           Caenorhabditis elegans.
                                                                                               AC006808
AC006808.1 GI:4263130
                                                                                       HTG.
                                                                                                                                                                                                                                             Similarity
(bases 1 to 34544)

Chases 1 to 34544)

C. elegans Genome Sequencing Consortium,

nome Sequencing Center, St. Louis U.S.A. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (29-JUN-2000) to the EMBL/GenBank/DDBJ databases.
t of Botany, The University of British Columbia, #3529-6270
y Blvd., Vancouver, BC V6T 124, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9MSC1; Q9MSC1
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                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                        BP; 591'A; 383
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origin of dinoflagellate chloroplast minicircular
                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:35672"
/organelle="plastid:chloroplast"
/organism="Heterocapsa pygmaea"
/strain="CCMP 1490"
826...1872
                                                                                                                                                                                                                                                                                                                                  VYPIGQGSFSDGMPLGISGTFNFMLVFQAEHNILMHPFHILGVAAVFGGSLFSAMHGSL
VTSSLVAETAGDLSLNVGYNFGQEDETYSISAAHGYFGRLIFQYASFNNSRSLHFFLAA
                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAG25876.1"
/translation="MKNTFNTSNVEANAYSFWGYVIGFILSTSNRLYIGWFGILMFPLL
/LATYNAYIAAFIFAPPUDIDGIREPVAGALLYGNNIISGAVIDSSNAIGVHFYPWEAL
GFDEWLYNGGTYQFVVLHFILGAGAYMGREWEFAFRLGMRPWIFVAFSAPLVAASAVFI
                                                                                                                                                                                                                                                                                                                        WPVIGIWFTALGVSTMAFNLNGLNFNQSIIDSSGHLINSWADIVNRADLGMEVMHERNA
                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/db_xref="SPTREMBL:Q9MSC1"
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                                                                                                                                                                                                                                                                                                                                                                                                     /product="psbA"
                                                                                                                              34544 bp
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     Washington University nd the Sanger Centre,
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MEDLINE
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Submitted (23-FEB-1999) Genome
University School of Medicine,
                                                                                                                                                                                                                 Direct Submission
Submitted (01-MAR-2000) Genome
University School of Medicine,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortiun Science 282 (5396), 2012-2018 (1998) 99069613
                                                                                                         Submitted
                                                                                                                            University, 4444 Forest
                                                                                                                                           Submitted (28-MAR-2000)
                                                                                                                                                             Waterston, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tin-Wollam, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erratum:[[published errata appear in Science 1999 1;283(5398):35 and 1999 Mar 26;283(5410):2103 and 3;285(5433):1493]]
                                                                                                                                                                                                                                                                                         Waterston, R.H.
                                                                                                                                                                                                                                                                                                                             MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence of C. elegans cosmid Y58G8A
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-Wollam, A., Graves, T. and Harrison, M.
              St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
Cambridge CB10 IRQ, England
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                         by:
                                                                    Department
                                                                                       Genome Sequencing Center
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                                                                    of Genetics, Washington University,
                                                                                                                        Department of Genetics, Park Avenue, St. Louis,
                                                                                                                                                                                                                                Sequencing Center, Washington 4444 Forest Park Parkway, St. Louis,
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Missouri 63108,
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                                                                                                                                                                                                                                                                                                                                             Louis,
                                                                                                                            USA
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NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

## NEIGHBORING COSMID INFORMATION:

This is a segment of the YAC Y58G8, sequenced to span the gap between R02C2 and F33E11. The 5' clone is R02C2, 3100 bp overlap; 3' clone is F33E11, 200 bp overlap. Actual start of this YAC is at base position 20847 of CELDC2; actual end is at 7365 of CELT22H9.

Sequence fidelity from base pair 6911 to base pair 9100 can not be guaranteed due to a tandem repeat. This region may contain misassemblies, single cloned areas, or regions of low quality.

## NOT THE

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation)

Location/Qualifiers

1. 34544

/organism="Caenorhabditis elegans"
/strain="Bristol N2"
/db\_xref="taxon:6239"
/chromosome="V"

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CDS
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/db_xref="G1:7332126"
/tcanslation="MILIRILSIGVLINFHFGNAASQSTDERKLEAQLLKGYNSKVRP
/kranslation="MILIRILSIGVLINFHFGNAASQSTDERKLEAQLLKGYNSKVRP
VKVESTVTQVAVYLNIAHVEKVDEHEQTALVHOHLMASWTDEYLKWERKATNISTLSI
ASSKLWQPALQLYNSARGNSWSLYLTGLPAIYYNTGKVWSRGTEFFFTTCQEPETNWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="contains similarity to Pfam family PF00065
(Neurotransmitter-gated ion-channel), Score=37.5,
E=3.2e-10, N=2; coded for by C. elegans cDNA yk304h6.3;
coded for by C. elegans cDNA yk304h6.5; coded for by C.
elegans cDNA yk468h10.3; coded for by C. elegans cDNA
                                                                                                                                                                         complement(23241. .24074)
/gene="Y58G8A.4"
                                                                                                                                                                                                                                                             TPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNA
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A1SLDKFLH1NDPTKQPVS1RQALA1TFL1W1VSTL1NLPYLMSFEHVDGSFYVQPGE
                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
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/db.xref="G1:7332128"
/translation="MSAALDEYIRSIFTELYGELFVLGIFGNGGVLWAVARNKRLQSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(20844. .22820)
/gene="Y58G8A.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKKMRKLEIQLLHIKRFAFFFVIFVYLFAILLVLAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLIVMSNFLRVRLPSHYEFDFGYDITEIPKKFGLTRFFTTKGLSFDPQELLNPAQLTS
EAEIQKEASTSIGISNPLAESGSDTDLLINLPKNSEADLSERSETLGMPDSEKTQKES
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SWKKHCYWGPKGCLDAEPDGNPDWYWSLLEFGITLKRHLPYFSLTIVMPMVSTSLMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PMRWNDSLRKEVTTRDAFGQVIQLWSTQA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKVEIRCPNTINIIIDDVNEYIYLGRQINDSNNLLPELHRRRAAWAAFTNIKSTIDQ
ITCPRLRANLFDSTVLPALIYGSEAWTFTKELAERVRVTHAALERKLVGLTLTEQRER
NIHREEVREKSKLRDPLIHIKKKKLGWAGHVARRTDGRWTTLMNDWCPRDEKRPVGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGDRESLENYRPICLLPVLYKTFTKCVLNRIRKTLEEAQPVEQAGFRRSFSTIDHIHS
VQRLLEVGREYQIPLTUFIDGKAFDSVEPQDVWGJLQQGYUQRGYINLQECYTDC
STTFTPFHKNTVTVPVIRGVRQGDFISPNLFSACLEHVFRGLNNKHFKGDERYETEGIS
VNGQNLTNLRFADDIVLVAHNPRTASQMLTELVEKCSSVGLKINTGKTKVLRNRFAYK
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INSFPNGKAAGSDKITADFLKSCGDNVIRLITGRFNRVLESGNIPKDWKTSKTTLIFK
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LANGKFVTDTSVLPSFTNGSDHRLLKSNVHFNINLAKLDQVKRRKPPKRVLEKATALA
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/protein_id="AAF60814.1"
/db_xref="G1:7332127"
/translation="MRKENEKLCTRRGDRNFEETQVSKYKLIIGDFNARVGNRKDENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="Y58G8A"
2379. .5358
/evidence=not_experimental
/product="Hypothetical protein Y58G8A.4"
/protein_id="AAF60816.1"
                                                                                                                                               complement(join(23241.
                                                                                                                                                                                                                                  QFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGLSFYLFFGKKNRSQLF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yk468h10.
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/gene="Y58G8A.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="contains similarity ot Pfam family PF00001 (7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(10191. .10218,10271. .10440,10953. .11104,11151. .1
11346. .11490,11940. .12106,12166. .12319,12367. .12556,
                                                                                                                    /gene="Y58G8A.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Y58G8A.3"
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                                                                                         codon_start=1
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8. .22244,22429. .22620,22807. .22820))
                                                                                                                                               .23565,23665. .23873,23982.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 6, constructed by the Sanger Centre Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requests: clonerequest@sanger.ac.uk
On Jul 19, 2001 this sequence version replaced gi:14329623.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                          IMPORTANT: This sequence is not the entire insert of clone RP11-320P15 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP11-100E6 is at 36226 in this sequence. The true right end of clone RP1-23916 is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as described unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                RP11-320P15 is from the library RPCI-11.2 of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                          http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 38225)
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FDAWLVRRPPERPEOPORLPPPSATLSOVIRTWARAFRSLRRLRHKASMILLCKFWVS
WMDFLTYNFOKNLSTFLTTKITISVIYORSHLFHPKPLERLVLKHENF*
$ 5567 c 6036 g 10748 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                             Location/Qualifiers
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/translation="MEIILCFLNYLAHFKAGFEIDLFNFINITIYKKFPFFFHRLKFD
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equence from clone RP11-320P15 on chromosome
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                                                                                                                                                                                                                                                      /note="MIR repeat: 28243. .28715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9330 .9451
/note="61 copies 2 mer tt 59% conserved"
                                                                                       'note="L1 repeat: matches 4734. .5064 of consensus"
                                                                                                                           'note="AluY repeat: matches 2.
                                                                                                                                                               'note="MIR repeat:
                                                                                                                                                                                      29991.
                                                                                                                                                                                                     'note="MLT1H repeat: matches 91.
                                                                                                                                                                                                                                     note="L1MA4 repeat: matches 5817. .6300 of consensus"
                                                                                                                                                                                                                                                                                                           note="Alux repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                             'note="MLT1A2 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MER89 repeat: matches 8. .557 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="AluSp repeat: matches 1.
                                                   'note="L1MC/D repeat: matches 5528, .5563 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                   note="MER57B repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="LTR16C repeat: matches 50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L2 repeat: matches 1035. .2358 of consensus"
13769. .14132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="LIM4 repeat: matches 2176, .4208 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MLT1A1 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="MER91 repeat: matches 1. .63 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6645. .16967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="THE1C repeat: matches 3. .359 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7690. .11001
"note="L1MEc repeat: matches 653. .2052 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .076. .1388
'note="L1MC1 repeat: matches 5883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="MLT1A1 repeat: matches 218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L1MC1 repeat: matches 6225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-320P15"
/clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MER20 repeat: matches 160. .214 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="L2 repeat: matches 2365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="L1MC1 repeat: matches 5219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1M4 repeat: matches 4735. .4952 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .20635
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                                     .32461
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 repeat: matches 3821.
                                                                                                                                                                                                                                                                                                                                    . 26391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 2665. .2700 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat:
                                                                                                                                                               matches 28.
                                                                                                                                                                                                                                                                             matches 46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matches 1. .364 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                   matches 42.
                                                                                                                                                                 .186
                                                                                                                                                                                                                                                                           .175 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .184 of consensus"
                                                                                                                             .311 of
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               .3954 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .305 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2710 of
                                                                                                                                                                                                                                                                                                                                               .374 of consensus
                                                                                                                                                                                                     .271 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                   .403 of consensus
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RESULT 39
SPCC16C4/c
LOCUS
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Best Local
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                                                                                                                                                                                                                             (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
During 1995 to 1996 about 66% of S. pombe chromosome 1 was
sequenced by the Sanger Centre. The sequencing of the S. pombe
genome is now being continued with funding from The European
Commission. Fourteen European sequencing laboratories, including
the Sanger Centre, are participating in the project.
Protein coding regions (CDS) have been predicted with the help of
computer analysis using the Genefinder program in PomBase (an ACEDB
database) with additional predictions for the branch-acceptor sites
supplied by the program Sp3splice. CAUTION: It is possible that for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conser
(complementary strand).
The more significant matches with motifs in the PROSITE are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
                                                                                                number of introns/exons or we may not have chosen the correct splice donor/acceptor sites.
CDS are numbered using the following system eg SPBC25H2.0lc. (pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA, E-mail: barrellesanger.ac.uk and Unite de Biochimie Physiologique, Universite Catholique de Louvain, Place Croix du Sud 2/20, B-1348 Louvain-la-Neuve, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein kinase; G-beta repeats; gene free region; Glucosamine-6-phosphate isomerase; low complexity gene free region; n-terminal acetyltransferase; peptidyl-prolyl cis-trans isomerase; pseudouridylate synthase; RNA binding protein; rna binding protein; rpl12.1; soll family protein; sts5; target of the inhibitor staurosporine; tf2 type LTR; TPR Domain; transcription factor subunit; transcription initiation factor tfiid 60 kd subunit; wD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-SEP-1998) European Schizosaccharomyces genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purnelle,B., Goffeau,A., Wood,V., Rajandream,M.A. and Direct Submission
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S.pombe chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Details of yeast sequencing at the Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60s ribosomal protein L12A; cdc2-cdc28 family serine-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tission yeast.
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                                                                                                                                                                                                             individual CDS we may have underestimated or overestimated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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6661 c 6907 g
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34424. .34729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cosmid c16C4
EM: AL033406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequenced clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSNRIGPQRSTKTAAKLRLLPSTEEFDDFRRQDTGREVYSQIPQ
IEGSTAKRDAEHLGKRHREELERVTAYCTCDTFRVDLLFKFFGSRRSSHKTRPKQFDE
CIYSPYSYNNEETTDLLPDTLESSRGTLNRESSQESLQSIFEESGLDRNQPLFREVFC
CTYGVVVLWGYTIDEEHRFLRELGRFEIEKLKLEDMEVEEFNYYITTLYQPRIFNDFI
ALRDASNYMIRLSISHAIAQSVKISLFEELVNETIDATKDTPQMIAETGRVNLKREEI
ALRDASNYMIRLSISHAIAQSVKISLFEELVNETIDATKDTPQMIAETGRVNLKREEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="DPKTLLHGCSKCGSLFIFGRNIKLRTISSERKARTDLKKGEVSR LGTNLEINCLYCSYVHEIPLGVPLRLH9SKQALRAKAIAESSSTKLESRKSAHNAKVK QRQRLRASGLNGILDRKKKKDEVAKSTSSLSLQDFMSPI"
join(1000. 1307,1391. 1656,1735. 1796,1877. 2581)
/gene="SPCC16C4.01"
join(1000. 1307,1391. 1656,1735. 1796,1877. 2581)
/gene="SPCC16C4.01"
/gene="
complement(join(3019. .3212,3265./gene="SPCC16C4.20c"
                                                                                                 /note="ctaacagatatag, splice branch and acceptor"
complement(join(3019. .3212,3265. .3292,3338. .33
/gene="SPCC16C4.20c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMAVGQLFILRININLQGSVLDSPELMWTEPQLEPIYTAARSYLEINQRVALLNQRVE
VIGDLLSMLKEQITHTHDESLEWIVVILMGLLVLIALFSIVVRLADGFKLNDFRLVIN
NSNKFILLFANTLFYIGGLEAVSITTEESFLFLHYVYIIEEMGKGKKIKPYLSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="conserved hypothetical protein"
/protein_id="CAA20740.1"
/db_xref="GI:3560255"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein_id="CAB71193.1"
/db_xref="GI:6855454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="SPCC16C4.19, len:>140, SIMILARITY:Saccharomyces cerevisiae, RMRP_YEAST, rnase mrp protein component sm (198 aa), fasta scores: opt: 142, E():0.0035, (26.0% identity in 146 aa)"
                                                                                                                                                                                                                                                                                                                                                                 /note="ttaacatttgtaatttttag, splice branch and acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1376. .1390
/note="ctaacattataacag, splice branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4896"
/chromosome="III"
/clone="cosmid c16C4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/label=SPCC16C4.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SPCC16C4.19"
/note="SPCC5E4.08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Schizosaccharomyces pombe"
/strain="972h-"
                                                                                                                                                                                                                                                                                          note="gtatga, splice donor sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="SPTREMBL:074446"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="SPCC16C4.19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "IIIL"=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtatgc, splice donor sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gttagt, splice donor sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   It may be shorter because we only sequence
                                                   .3292,3338. .3349))
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                                                                                                                                               .3349))
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/note="possible gene free region, low complexity, SPCC16C4. 14c and SPCC16C4.15c are predicted in t region, but have very low coding potential and no
                                                                                                                                                                                                         /note="Match to PF00639 Rotamase, Score 138.03"
                                                                           7366. .7381

/note="ctaacactatgtgtag,

/note="ctaacactatgtgtag,
                                                                                                                                                                                                                                                                                                                                                                                                                        VVETSSGFHIIQRHA"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mSNTGLPKPWIVKISRSRNRPYFFNTETHESLWEPPAATDMAAL
KKFIANELQESVTPTEASNSPKIRASHLLVKHRESRRPSSWKEEHITRSKEEARKLAE
HYEQLLKSGSVSMHDLAMKESDCSSARRGGELGEFGRDEMQKPFEDAAFALKPGEISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="peptidyl-prolyl cis-trans isomerase.
/protein_id="CAA20742.1"
/db_xref="GI:3560257"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCECY EVLGLL I RYLCENCDVLAQR I EPDKFFQLQRSLTELFSDTMDFLRDAWDNNKN
RDNLASHVTV I SAVATLCLWLTEDDSQYAQASGLMD I FVYLWRHSWSNG I DYAKWI SV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLC IPVICTLSSNPKSAKYLLYYTSFI I NEFPFEQAFEILSNALYALDNVQTYMRPIF
QGIDKRRGWKLDCTFSFFSDLFSRFPVQSWYSEA I RANLQPLMDAVVERFITDKNLSS
ATVILSNLLKAAGPAS IMPNDGFMILVIGRCSAE I RGSLGMLVKAVGQKGKHGTVSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(4510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="gtagga, splice d
complement(4510..6156)
/gene="SPCC16C4.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="ttgaccgcgtag, splice branch and
complement(3332. .3337)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(3293.
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VERDIQRYRHEAQLLSKVLEKKGLNKEKEAGET"
                                                                                                                                                                                                                                                            join(7025. .7236,7382. .7505)
/gene="SPCC16C4.03"
                                                                                                                                                                                                                                                                                                                                                                  5851. .6943
/gene="SPCC16C4.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SPCC16C4.03, len:175, SIMILARITY: Emericella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(6836. .7236,7382. .7508)
/gene="SPCC16C4.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQAIQDFHILIQLNSLVPQSIWNDDIWQEPYWKNLLESNF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALPSMLSNKVFFKAFKDFDAWKVVYDDF1KCNDDLKGDKSFNDY1LSTNEEDGEDERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WERMDMKFLDRLLLSTHYEYVDLGVSILLAFCSEEAILRSYEVKKRVSTLLQCCLKHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVTDKDEDSNASGESRGSMELLENCFSLLHAQDDTSKFVSLTMLAKLLNDHPNLIFKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:074447"
/translation="MHIPHFHLHKGPKGVRTISYEQLLSEDDSYASEKLSEDHVTEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
/protein_id="CAA20741.1"
/db_xref="GI:3560256"
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/protein_id="CAB71194.1"
/db_xref="GI:6855455"
                                                                                                                                                         note="gtatgt, splice donor sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:074448"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=SPCC16C4.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=SPCC16C4.02c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="SPCC16C4.02c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SPCC16C4.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="gtgtgt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=SPCC16C4.20c
                                                                                                                                                                                                                                                                                                                                             'note="Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    836. .7236,7382. .7508)
"SPCC16C4.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , 042735, peptidyl-prolyl cis/trans isomerase.,
f asta scores: opt: 666, E():0, (57.5% identity
                                                                                                                                                                                                                                                                                                                                          to PF00397
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93. .3304)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6156)
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                                                                                                      splice branch and
                                                                                                                                                                                                                                    PPIC-type PPIASE domain.
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                                                                                                                                                                                                                                                                                                                                                domain Score
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REFERENCE
AUTHORS
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KEYWORDS
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AC020579/c
                                                  FEATURES
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AC020579
AC020579.5
HTG.
                                                                                                                                                           similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as
                                                                                                                                                                                                                                                                         http://www.tigr.org/softlabb/glimmerm_htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-JAN-2001) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Jan 19, 2001 this sequence version replaced gi:12280787. Address all correspondence to:at@tigr.org
                                                                                                             hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
                                                                                                                                                                                                                                similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST
                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html)
                                                                                                                                                                                                                                                                                                                                                                                                              prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GenemarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes were identified by a combination of several methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAC clone F1017 is from Arabidopsis thaliana chromosome 1 The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Town, C.D. and Kaul, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-JAN-2000) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 50821)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin,X., Kaul,S., Town,C.D., Benito,M., CreasyT.H., Haas,B.J., Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii;C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 1 BAC F1017 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana
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17; Conserv
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                                                                                      repeats are identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
/organism="Arabidopsis thaliana"
                                             Location/Qualifiers
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/gene="SPCC16C4.04"

join(9339. .9601,9647. .9851,9905.

/gene="SPCC16C4.04"
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complement(12470. .12501)
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complement(3045. .13067)
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join(<13093. .14242,14327. .
15941. .16423)</pre>
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13993. .16423
/gene="F1017.2"
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from [Arabidopsis thallana]"
join(13093. .14242,14327. .1450p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10576. .10693,
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/codon_start=1
                                                                                                                                                                                                                                       complement(join(16481. .17251,17318. .17587))
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                                                                                                                                                                                                                                                                                                                                                                              complement(16481.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAALDYILAESYDPVYGARPIRRWMEKKVVTELSKMVVREEIDENSTVYIDAGAGDLV
YRVESGGLVDASTGKKSDVLIHIANGPKRSDAAQAVKKMRIEEIEDDDNEEMIED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDENLLVRIDMSEYMEQHSVSRLIGAPPGYVGHEEGGQLTEAVRRRPYCVILFDEVEK
AHVAVFNTLLQVLDDGRLTDGQGRTVDFRNSVIIMTSNLGAEHLLAGLTGKVTMEVAR
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DLRDKLQPLTMKYRKEKERIDEIRRLKQKREELMFS/LQEAEKTOLARAADLRYGAIQ
EVESSAIAQLESTSSEENVMLTENVGEBHIAEVYSKWFGIPUTRLGQNEKERLIGLDS
LHKRVVGQNQAVNAVSEAILRSRAGLGRPQQPTGSFLFLGPTGVGKTELAKALAEQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIDEIHLVLGAGKTEGSMDAANLFKPMLARGQLRCIGATTLEEYRKYVEKDAAFERRF
QQVYVAEPSVPDTISILRGLKEKYEGHHGVRIQDRALINAAQLSARYITGRHLPDKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mnpekfthkTnetlaTaheLavnaghaQftpLhLagaLISDpTg
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RGDTHLAVDQLIMGLLEDSQIRDLLNEVGVATARVKSEVEKLRGKEGKKVESASGDTN
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FDKPGYGESDPDPIRTPKSLALDIEELADQLSLGSKFYVIGKSMGGQAAWGCLKYTPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCVMREVRKHFRPELLNRLDEIVVFDPLSHDQLRKVARLQMKDVAVRLAERGVALAVT
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/gene="F1017.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQALKTYGRDLVEQAGKLDPVIGRDEEIRRVVRILSRRTKNNPVLIGEPGVGKTAVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="heat shock protein 101; 13093-16240"
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/protein_id="AAG52400.1"
/db_xref="GI:12324898"
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/db_xref="GI:12324908"
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .14242,14327. .14508,14649. .15274,15359. .15836
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Query Match
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/db_xref="GI:12324901"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to unknown protein GB:AAD21437
[Arabidopsis thaliana]"
complement(join(21829. .22626,22877. .23197))
/gene="F1017.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="unknown protein; 21119-18687"
/protein_id="AAG52412.1"
/protein_id="AAG52412.1"
/db.xref=="G1:13234910"
/translation="MASDSSRKSSLKPSSRKSFLFPSVVIVIVGIIVALTVQSKLKPP
/translation="MASDSSRKSSLKPSSRKSFLFPSVVIVIVGIIVALTVQSKLKPP
OPKLCGSSSGPPITAPRIKLODGRYLAVKEHGLFREKANRKIVIVHGISCKCRYNGFA
TLLSPDLVEELGVYMVSTDRPGVCSSDPHPSRFUVSDIEBLDDQLSGSKRYVGR
TLLSPDLVEELGVYMVSTDRPGVGKDQWAV
                                                                                                                                                                                                                                                                                                                                                                                                   EVNWYKGKRMAY IYKAKTKKNGSHYRC IWGKVTRPHGNSGVVRAKFTSNLPPKSMGSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(<23489. .23520,23750. .23785,24176. .24404,24499.
/gene="F1017.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESINRDMIVGFGNWEFGPLDLENPFLNKEGSVHLWQGDEDMLVPAKLQRYLAHQLPWV
HYHEVPRSGHFFHYIKGVVDDIVKSLLTSDVRASRVCI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MTRDSSRNSSLKPMPRKKFLFPSVVIVIVGIIVAFTYQSKLKPP
PKLCGSSGGPPITAPRIKLODGRYLAVKEHGLPREKANRKIVE HGSDCCRHDAVFA
TLLSPDLVEELGVYMVSFDRPGYCESDPHPSRFPRSLVSDLEELADQLSLSGSKFYVLG
YSMGGQAAMGCLKXIPHRLAGVTLVAPVVNYXMKNLPLNVSTEGFNFQQKRDQLAVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="unknown protein; 23197-21829"
/protein_id="AAG52399.1"
/db_xref="GI:12324897"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HES I NRDMIVGFGNWEFDPLDLDNPFLNNEGFVHLWQGDEDMLVPVKLQRYLAHQLPW
VHYHEVPRSGHFFHFTKGVVDNIVTTLLTTDTDT I RQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVAHYAPWLIYWWNTQKWFPGSSIANRDSLLSQSDRDIISKRGYTRKPHWAEVRQQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(18687. .19284,20351. .20547,20799.
/gene="F1017.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(18687. .21119)
/gene="F1017.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(<18687. .19284,20351.
/gene="F1017.4"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"putative ribosomal protein; 23489-24540"
/protein_id="AAG52401.1"
/db_xref="GI:12324899"
/translation="MVKGRQGERVRLYVRGTTLGYKRSKSNQYPNTSLVQIEGVNTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(21829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(<21829. .22626,22877. .>23197))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLELENPFLNREGSVHLWQGDEDMLVPVTLQRY IADKLPWLHYHEVAGGGHFFPLAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLAGVTLVAPVVNYYWRNLPLNISTEGFNLQQKRDQWAVRVAHYAPWLIYWWNTQNWF
PGSSVVNRDGGVLSQPDKDIILKLGSSRKPHLAEVRQQGIHESINRDMIVGFGNWEFD
                                                                                                                                                                                                                                                                                                                                 29144. .>29950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               јотн (23489. . 23
/gene="F1017.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to ribosomal protein L33B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F1017.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AHYTPWLIYWWNTQKWFPGSSIANRDHSLLAQPDKDIISKLGSSRKPHWAEVRQQGIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to unknown protein GB:AAD21437 from
[Arabidopsis thaliana]"
                                              translation="MLLQRSSMSQLWGSVRMRTSRLSLNRTKAVSLRCSAQPNKPKAA/
                                                                                                                                                                                                                                                              /gene="F1017.7"
                                                                                                                                                                                                                                                                                                        /gene="F1017.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(23489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="F1017.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F1017.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F1017
                                                                                                                                                                                                                                 note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=]
                                                                                                                                                                                                                                                                                                                                                         (<25509.
  13.8%;
                                                                                                                                                                                                                                                                                     29950
  Score 17;
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                                                                                                                                                                                                             25911,25995.
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                                                                                                                                                                                                                                      GB:KIAA0361
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  DВ
                                                                                                                                                                                                             .26563,26663.
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  8
                                                                                                                                                                                                           from [Homo sapiens]"
563,26663. .29047,29144.
Length 50821;
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                                                                                                                                                                                                             .29950)
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
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AC018376
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 taagtttcacatgtaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehozzky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrin, J., Morrow, J., Naylor, J., Norman, C.H., O'Connoor, T., O'Donnell, P., Peterson, K., Pierre, N., Pollara, V., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced gi:6554602. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavkly,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
AC018376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collins,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens, clone RP11-3P5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                         sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                       will be sequenced to completion. In the event th
the record is updated, the accession number will
                                                                                                                                                                                                                                                         However,
                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This record contains 60 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 59935)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 59935)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L28 Center clone name: 3_P_5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center
                                                                                                                                                                            preserved.
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                                                             1921: contig of 906 bp in 1922 2021: gap of 100 bp
                                                                                  916 1015: gap of 100 bp
1016 1921: contia of 000
. 3030: gap
1 3907:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                    it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collymore, A., Cooke, P., DeArellano, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59935 bp DNA clone RP11-3P5,
                                                                                                                                                                                                  is updated,
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                                                  2930:
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Primates;
of 100 bp
contig of 877 l
                       contig of 909 bp in length of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L2801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
bp in length
                                                                                                                                                  bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for Genome
                                                                                                                                                                                                                                 that
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length

length

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6015
6933 7032: gar
7950: ,
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27009 27108: gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . gap
5914:
5 6014: gap o.
6932:
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Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K17E12.
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48115: contig o
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5059: gap of 100 bp
55924: contig of 865 bp 1
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49922: contig of 8
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Sato, S., Nakamura, A.,
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contig of 914 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 919 bp
                                                                                                                                                 (strain:Columbia) DNA, clone_lib:Mitsui TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of
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Mismatches
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Asamizu, E. and Tabata, S.

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FEATURES
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MEDLINE
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                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
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For the latest information on annotation of this clone, please see

http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=K17E12

Genes with similarity to proteins in the databases are described in

product or 'note' qualifiers. Genes that have no significant

protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail

(Informatics Group, Oak Ridge National Laboratory,

http://compilo.ornl.gov/Grail-1.3/),

BENSCAN (Chris Burge, MIT, http://ccR-081.mit.edu/GENSCAN.html),

RetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of

heneary http://ccm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (28-JUL-1999) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:Ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone.
shorter because we remove overlaps between neighboring sul
The 5' clone is MYF5 and the 3' clone is K1G2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel), Stanford University, http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, televice of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695\ \mathrm{bp} regions covered by 90 Pl, TAC and BAC clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko, T., Kato, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 7 (3), 217-221 (2000)
20363099
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                                                        complement(join(9327. 10950. .11091))
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                                                                                                                                                                  VGHCEQGMKIKVNVVSSDSKSASSPSGSGSGSGSGSGSGSGSGHGLRASTGYMFVVGS
LVIGLIWAY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIVTSEIDQCLNEEFRVIPGLGEFGDRYFGTDE"
complement(join(7607. .7950,8044. .8209))
/note="gene_id:K17E12.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSNSSFATIDDPAAPHOFFVIGVTGGTASGKTTVCDMIIQQLHDHRIVLVNQDSFYRG
LTSEELEHVQEYNFHHPDAFDTEQLLHCVDLIKSGQPVQIPIVDFKTHQRKVDAFRQV
NACDVIILEGILVFHDSKTVRDLMNKLIFVDTDADVRLARRIIRBDTVERGRDVDSVLEQ
YAKFVKPAFDDFVLPSKKYADVIIPRGGDNHVAVDLIVQHIHTKLGQHDLCKIYPNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIETTFQIRGMHTLIREKDISKHDFVFYSDRLIRLVVEHGLGHLPFTEKQVVTPTGSV
YSGVDFCKKLCGVSVIRSGESMENALRACCKGIKIGKILIHRDGDNGMQLIYEKLPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="uridine kinase-like protein"
/protein_id="BAB02114.1"
/db_xref="GI:9294212"
                                                                                                                                                                                                                                                                  /translation="MKMQAVLVILVFSGLLSVKTALAARHVIGGSQGWEQSVDFDSWS
SDQSFKVGDQIELHSVVELGSETAYKSCDLGTSVNSLSSGNDVVKLSKTGTRYFACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
/protein_id="BAB02115.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:9294213"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MPEDSTAIDYVMEKASGPHFSGLRLDGLLSSPSKSSVSSPSHFR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="gene_id:K17E12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Mitsui TAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SERHVLLLDPVLGTGNSANQAIELLIQKGVPEAHIIFLNLISAPEGIHCVCKRFPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .63604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6786))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato, S., Nakamura, Y., Asamizu, E. and Tabata, S.
                                                                                                          .9715,9806. .9886,10692. .10784,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submissions
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
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complement(join(20013. .20129,20428. .20493,20594. .20710
20791. .20862,20950. .21229,21627. .21838,22180. .22239))
//note="gene_id:K17E12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="ubiquinol-cytochrome c1 reductase cytochrome c1 precursor-like protein" protein_d="Bab02119.1" protein_id="Bab02119.1" /db_xref="G1:9394217" /db_xref="G1:9394217" /db_xref="MVGGGVIQQILRRKLHSQSLATPVLSWFSSKKAHEDAGSSGVRA/translation="MVGGGVIQQILRRKLHSQSLATPVLSWFSSKKAHEDAGSSGVRALLLGAGVTGLLSFSTVASADEAEHGLESPEYPWPHDGILSSYDHASIRRGHQYYQQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGQKLILRACEPLPRRRCLAKTYQKQDLSKSPDSLWRSYSNKSYNWSGLGCKSFDCLK
GKKLSKECYGCFDLGVEKDRFYKYKGKNDFLIDDYLGLGSGKIRIGFDISGGSGTFAA
RMAEKNYTYITNTLNNGAPFSEFIAARGLFPLFLSLDHRFPFLDNYFDLIHASSGLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mankpdhhhhhhySsrrlmLvlyftSvlGIGFIAAFLCLSSSIP
$V$AVESIWVPVNRPELQIPIILDXKJYQKRSKQSUDYHSHVDYNFTDNKWGIFADIPAPELKW
EEMESAPVPRLDGYSVGINULLYVESGYGSLDVYHSHVDYNFTDNKWGIFADIPAPELKW
ANSHLGIVTDGRYVYVVSGQLGPQCRGPTSRSFVLDSFTKTWLEFPSLPAPRYAPATQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MGSSSSSSSLNNSPIRADSMYTPESQMTVNDNKNDNVSILSPSVK
KSFESPRKSTSIPANNNLTPVKSRWSFSSSKKSFGSKDETFFDSQPWLQSDSDDDFHS
VNGDFTPSLGNTPKSSFSDRPPRFHNLIFHEKKPSRGSSSPAPLPRRKKLGELFRDSI
                                                                    VWLVAEEATAAMHCNYQAFTCRVRMQYTWKETKYTKTVPCDVWKMEFGGFAWRLDTTA
                                                                                                           ADNNNNSSYGMSKRTKRKYVRVSKNNKGTCRGKSRSDLSDDREQTDVVTLQLLPEKSD
ISGEYSPLDQDSLDPSVKSIIGEETQETNTWGMFNGSVTAEMETWVTVESVTSVCEGS
LSSHAVGITDVEIVDNLGKDTCPAFVSDGSNRVVWVNEAYRRNVSGDDSTASVSPEVV
                                                                                                                                                                                                                                                    /evidence=not_experimental
/protein_id="BAB02120.1"
/db_xref="GI:9294218"
                                                                                                                                                                                                                                                                                                                                                                                                     similar to unknown protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                        gene_id:K17E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FPGGA IAMPKMLNDEAVEYEDGVPATEAQMGKDIVSFLAWAAEPEMEERKLMGFKWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CASCHSMSLISYRDLVGVAYTEEEAKAMAAEIEVVDGPNDEGEMFTRPGKLSDRFPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KADAQVYLSAVLQKPVRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSHSQANSPLLHSSNNISLVSQHLSLILREIDSSQRKLAQMEKQMLGYESIDISRPNI
VPELKLFLQRHQLPLGKDSRTGITEMVSSVGHSCGKSTDLLSQYMSYKVFDRCPDDWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
/protein_id="BAB02118.1"
/db_xref="GI:9294216"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene_id:K17E12.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGYLYFTSGQRDRGPDNPQPGKVIGEMWRTKLKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WIIVNNSIVIVGGTTDWHPYTKRLVLVGEIFRFQLDTLTWSVIGRLPYRVKTAMAGFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IWRGRLHYMGGSKENRNAVAFDHWSIAVKDGKALDEWREEVPIPRGGPHRACVVANDK
LLVIGGQEGDFMAKPNSPIFKCSRRREIFNGEVIMMDEEMKWKMLPPMPKNNSHIESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
/protein_id="BAB02117.1"
/db_xref="GI:9294215"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(15611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene_id:K17E12.3
similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YANESAARFANGGAYPPDLSLITKARHNGPNYVFALLTGYRDPPAGISIREGLHYNPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="emb|CAB62340.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLSLALLQAAYYRRLKWSVLKSRKLVLDVVN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
                                                                                                                                                                                                                      translation="MDQDDWLGTLRYAGKAQDKVSVDALMLRYRPIAPKPTTGQPCGV/
                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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.33512,33590. .33632,33728. .33790,34020. .34090
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.17074,17245.
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Collins,S., Collymore Domino,M., Doyle,M., Forrest,C., Gage,D.,
                           Boguslavkiy,L., Boukhgalter,B., BLOWN,A., COLLINS,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Collins,S., Collymore,A., Terreira,P., FitzHugh,W.,
                                                                                        Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
AC018413
                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                    Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome, clone RP11-17M16
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC018413.3 GI:12084068
HTG; HTGS_PHASE0.
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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GSSEDQSDDAKPMVQGDSSKLVNLQMPETANSEAQRDENTRIDDLFVGSQSTGALEQM
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FESSKETMTSTPNITLMKQCDTLLRKLWSHPHSWVFQAPVDVVKLNIPDYLTTIKHPM
DLGTVKKNLASGVYSSPHEFAADVRLTFTNAMTYNPPGHDVHIMGDILSKLFEARWKT
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/note="gb|AAC49691.1
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GGDSLFAAHHLAVLFVFLTCRYMVAHGACALLALLVVAEATSACQNTWTLADARGKDA
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/protein_id="BAB02122.1"
/db_xref="GI:9294220"
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unknown protein"
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LYMKQDDGEEEEPEAPVVPKPNETSLERPVDAFGSFNLKGSNPLEQLGLYMKQDDDEE
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REAARQALLKMEKTVEINENSRFLEDLEMLSSSAPEQLPSSAEETSPERPLDALGSFN
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ARKCIMLNSNDEDPYGVQRQVISLYNMSQSERKDLIYRLKLELEQTKIVLKNAELQRM
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/protein_id="BAB02121.1"
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35378 .35520,35718 .36272)
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s clone RP11-17M16, LOW-PASS SEQUENCE SAMPLING.
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VERSION KEYWORDS

DEFINITION **LOCUS** AC018413/c RESULT

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SOURCE

ORGANISM

REFERENCE

AUTHORS JOURNAL REFERENCE

AUTHORS TITLE

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Submitted (10-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 12, 2001 this sequence version replaced gi:9123871. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Morrow, J., Naylor, J., Norman, C.I., O'Connor, T., O'Donnell, P., Peterson, K., Pierre, N., Pollara, V., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Rothman, D., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,
Karatas,A., Klein,J., Landers,T., Lehoczky,J., Lieu,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This record contains 80 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            overlap relationships among clones to be deduced. However, it should not be assumed that this clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved.
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Center clone name: 17_M_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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                           13951: contig
13952 14051: gap of
14052 14777: contig
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13135 13234: gap
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12338 12437:
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7311 7410: gap of 100 bp
7411 819: contig
3150 8240
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2476 3224: cor
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1649 2375: co
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9822: contig of 729 bp
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23 10654: contig of 732 bp
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5 11498: contig of 744 hr
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4044: contig of 7
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13951: cont
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12337: cont
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139b of 100 bp
1337: contig of 739 bp 1
139b of 100 bp
134: contig of 697 bp 1
134: contig of 717 bp 1
951: contig of 717 bp 1
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18019

15694: gap of 16405: con 16505:

contig of

17186: cont

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19669 19768: gap of 100 bp
19769 20505: contid of 737 bp in length
20506 20605: gap of 100 bp
21441 22450: contid of 735 bp in length
22151 22250: gap of 100 bp
22251 22981: contid of 731 bp in length
23982 23081: gap of 100 bp
23983 23912: gap of 100 bp
24632 24731: gap of 100 bp
25560 25459: contid of 731 bp in length
25560 2559: gap of 100 bp
26221: contid of 728 bp in length
26322 27049: contid of 662 bp in length
26322 2631: contid of 662 bp in length
26322 26321: gap of 100 bp
27050 27149: gap of 100 bp
27150 27149: gap of 100 bp
27186: contid of 728 bp in length
26322 27049: contid of 737 bp in length
27987 28808: gap of 100 bp
28709 28808: gap of 100 bp
28709 28808: gap of 100 bp
28709 29536: contid of 722 bp in length
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30364 30463: gap of 100 bp
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42749 43483: contig of 735 bp

43484 43583: gap of 100 bp

43584 44321: contig of 738 bp

44322 44421: gap of 100 bp

44422 45147: contig of 726 bp
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9019 18118: gap of 100 bp
1119 18843: contig of 725 bp in length
844 18943: gap of 100 bp
144 18943: gap of 100 bp
146 19668: contig of 725 bn (-
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02 41017: contig of 716 bp in 1
18 41117: gap of 100 bp in 1
18 41820: contig of 703 bp in 1
21 41920: gap of 100 bp in 1
21 41920: gap of 728 bp in 1
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     L Unpublished

L Disses 1 to 65998)

E 2 (bases 1 to 65998)

8 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

8 Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkly, L.,

8 Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkly, L.,

8 Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M.,

Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R.,

Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,

Marwan, D., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,

Marwan, D., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,

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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-287J24
Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE0.
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McEwan,P., McGurk,A., McKernan,
Meneus,L., Mihova,T., Miranda,C
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53443 53442: gap of 100 bp
53443 544212: contig of 770 bp in length
54213 5312: gap of 100 bp
54213 55140: contig of 728 bp in length
55041 55140: gap of 100 bp
55141 55860: contig of 728 bp in length
55961 5960: gap of 100 bp
55961 55960: gap of 100 bp
5603 57556: contig of 742 bp in length
57557 5656: gap of 100 bp
57557 57656: gap of 100 bp
58387 58486: contig of 730 bp in length
58387 58486: gap of 100 bp
59224: contig of 738 bp in length
58487 59224: contig of 738 bp in length
59225 59324: gap of 100 bp
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065: gap of 100 k
46816: contig of 751
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24481 24580:

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1478: gap of 10 26278: contig of 8 3378: gap of 10 27162: contig of 7

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19247:

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21922: gap of

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Submitted (16-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6980301. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Traylio, J., Vassiliev, H., Viel, R., VOA., Wilson, B., Wilson, B., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                will be sequenced to completion.
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9482 9581: gap of 100 bp

9582 10290: contig of 709 bp

10291 10390: gap of 100 bp

10291 1174: contig of 784 bp

11175 11274: gap of 100 bp

11175 1266: contig of 792 bp
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Contact: sequence_submissions@genome
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: L5205
Center clone name: 287_J_24
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3 7701: contin ~
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12931: contig of 765 bp it

13031: gap of 100 bp

13781: contig of 750 bp in

13881: gap of 100 bp

14655: contig of 774 bp

1755: gap of
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755: gap of 100 bg
15591: contig of 836 k
691: gap of 100 bg
16473: contig of 782 k
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                                                                                                                                       Grand-Plerre, N. Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Plerre, N. Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marcarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McHeeters, R., McCarthy, T., Naylor, J., Morman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Rogov, P., Rothman, P., Rogov,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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202 57301: gap of 100 bp
102 58058: contig of 757 bp in 1ε
59 58158: gap of 100 bp
59 58158: gap of 100 bp
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77 50036: gap of 100 bp
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      Theodore, J., Tirrel
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                                                                                                                    Schauer,S.,
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                                                                                                                    Severy, P.,
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B., Heaford,A., Horton,L.,
                                                          Subramanian, A.,
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Submitted (30-MAR-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overlap relationships among clones to be deduced.
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15150 15927: contig of 778 bp
15928 16027: gap of 100 bp
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066 7165: gap of 100 bp
66 7959: contig of 794 bp in
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60 8837: contig of 778 bp
38 8937: gap of 100 bp
38 934: gap of 1797 bp
35 9834: gap of 100 bp
35 10632: contig of 798 bp
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694: gap of 10
19501: contig of 8
601: gap of 10
20369: contig of 3
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9634 39733: gap of 100 bp

9734 40532: contig of 799 bp in length

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0633 41403: contig of 771 bp in length
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19 34418: gap of 1
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23026: contig of
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21294: contig of
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29924: contig of 790 bp
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30801: contig of 777 bp
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25622: contig of 7
722: gap of 1
26497: contig of
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36068: contig of 770 bp
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36970: contig of 802 bp
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28156: contig of 1:
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Best Local Similarity 100.0 Matches 17; Conservative	Query Match	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
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vative 0; Mismatches	13.8%; Score 17;	60922 61021: gap of 100 bp	9	60149: gap of 100 bp	60049: contig of 786 bp	59263: gap of 100 bp	ю О	58376: gap of 100 bp	58276: contig of 791 bp	57485: gap of 100 bp	57385: contig of 792 bp	56593: gap of 100 bp	56493: contig of 794 bp in length	55699: gap of 100 bp	55599: contig of 799 bp	54800: gap of 100 bp	54700: contig of 777 bp in length	53923: gap of 100 bp	53823: contig of 808 bp in length	53015: gap of 100 bp	52915: contig of 797 bp in length
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Gaps

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Search completed: March 19, 2002, 11:05:47 Job time: 4021 sec

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Result
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DNA encoding OMP-1
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AAC87998	AAF10271	AAC01762	AAF66405	AAF66301	AAF66728	AAC22215	AAX40689	AAC74896	AAH67192	AAZ14187	AAA01492	AAC13255	AAZ36299	AAC65362	AAV72819	AAC65347	AAV72858	AAC91627	AAX23517	AAC91677	AAC91676	AAC91675	AAC91674	AAC91672	AAC91671	AAC91670	AAC91600	AAH33277	AAC78084	AAC98971	AAQ47075	AAA38324	AAA38323
Human CLASP-2 geno	Fusarium venenatum	Human secreted pro	Novel human polynu	human	Novel human polynu	Human secreted pro	Human secreted pro	Human ORFX ORF451	C glutamicum codin	Human gene express	Human colon cancer	Human secreted pro	Mechanical stress	Human TDO2 gene G	Tryptophan 2,3-dio		Tryptophan 2,3-dio	Human angiotensino	Human kidney amino	Human angiotensino				cancer asso	Human pancreatic c	н		Human angiotensino					

## ALIGNMENTS

09-MAR-2001

(first entry)

AAC98121;

AAC98121 standard; cDNA; 464

ВP

**\_** 

Human colon cancer antigen nucleotide sequence SEQ ID NO:131

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RESULT AAC99121 ID AAC9 XX AAC9 XX AAC9 XX Hume XX Hume KW Idee KW Inem KW rep KW rep KW rep XX Inem X Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatle; cardioactive; neuroprotective; vulne; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss. WPI; 2000-587534/55. P-PSDB; AAB53364. Rosen CA, (HUMA-) HUMAN GENOME SCI INC 12-MAR-1999; 08-MAR-2000; 2000WO-US05883 21-SEP-2000 WO200055351-A1 Homo sapiens. Ruben SM; 99US-0124270. neuroprotective; vulnerary; renal disorder;

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RESULT 2
AAH29882/c
ID AAH298
XX
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AC AAH298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Called human colon cancer antigens, given in AAB53234 to AAB54006. The called human colon cancer antigens, given in AAB53234 to AAB54006. The chuman colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, cultivative, and cancer antigen polynucleotides, and cancer antigen polynucleotides, and concer antigen polynucleotides, and concer antigen polynucleotides, cultivative, such as colon cancer. The cultivative and antibodies to the proteins are useful for the prevention, cultivative that antiquosis of colon disorders, such as colon cancer. The colon concerning the proteins are useful for the proteins are useful for the proteins cultivative disorders, muscular disorders, reproductive disorders, immune cultivative disorders, infectious cultivative disorders, infectious cultivation, and candiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present concerning the proteins are used in the exemplification of the present concerning the proteins.
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Best Local S
Matches 18
                                                            disorders, yeast
certain diseases
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                                                                  deast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative lisorders, yeast and fungal infections, or for preventing apoptosis in sertain diseases .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          albicans apoptosis associated coding sequence #26
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           17;
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     Fig
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mmune disease; ischaemia; neurodegeneration;
                                                                                                                                                                                                                                                                                      De Backer MD,
Reekmans RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                              99EP-0870141
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        218pp;
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lon cancer -
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Pred. No.
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RESULT ANABA1461 ID ANABA1461 I
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                                     The present invention describes methods of obtaining immunogenic proteins from Nelsseria genomic sequences. AAA81453 to AAA82144 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81309 and AAA81304 represent PCR primers used in the isolation of Nelsseria meningitidis DNA sequences; and AAA81322 to AAA81259 and AAA81304 to AAA81305 represent PCR primers used in the isolation of Nelsseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodi against them, can be used in the manufacture of a composition. The
                                                                                                                                                                                                                                                                                                                                      Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleotide sequences of Neisseria meningitidis which can used in the diagnosis and treatment of N. meningitidis infection \epsilon other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identity treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaen and neurodegeneration. The present sequence is one of the C. albicans
composition medicament)
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Masignani V,
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30-APR-1999;
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                        can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pizza M;
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be used as a medicament
treating, preventing or
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C, Mora
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection;
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Ratti G,
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  (or in the manufacture of diagnosing infection due (
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2.1;
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Scarselli
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08-OCT-1999;
28-FEB-2000;
sequences which overlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the
                                                            The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                             Pizza M, Hi
Galeotti C,
                                                                                                                                                  Claim 7;
                                                                                                                                                                              Neisseria meningitidis B full length frames are used to detect, treat and
                                                                                                                                                                                                                               WPI; 2000-647603/62
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                                                                                                                                              Appendix A; 692pp; English.
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                                                                                                                                                                                                                                                                             Hickey E,
C, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      meningitidis; Neisseria gonorrheae; immunogenic; vaccine;
antigen; detection; infection; gene therapy; antibacteri
                                                                                                                                                                                                                                                              Grandi G
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99WO-US23573
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Ratti G, (
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Scarselli M,
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                                                                                                                                                                              genome sequence and open reading
prevent Neisserial infections -
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Scarlato V,
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                                                                                                                                                                                                                                                                             Rappuoli R;
                                                                                                                                                                                                                                                                                             Masignani V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                              09-OCT-1998;
30-APR-1999;
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                                                                                                                                                                                                                                        Rappuoli R,
                                                                                                                                                                                                                                                                     Frazer CM,
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                                                                                                                                                                                                                                                      Masignani V,
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                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis; Neisseria gonorrheae;
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99US-0132068
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                                                                                                                                                                                                                                                      Peterson
C, Mora
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome DNA sequence
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Ratti G, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome; immunogenic;
                                                                                                                                                                                                                                                       Scarselli
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic Topresent sequences; AAA81303 and AAB35620 to AAA825663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254

Isolated nucleotide sequences of Neisseria meningitidis which can used in the diagnosis and treatment of N. meningitidis infection other Neisserial infections, for example, N.gonorrhoea -

n be and

Claim 7; Page 866-1272; 1760pp; English

Neisseria DNA sequences and their corresponding proteins; AAAAAB1259 and AAAAB1304 to AAA81321 represent PCR primers used isolation of Neisseria meningitidis DNA sequences; and AAA813

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                                                                                                                               The present sequence is part of an essential gene from Drosophila melanogaster. Lack of expression of the protein encoded by this gene leads to a lethal or semi-lethal phenotype. The invention relates to 902 nucleic acid sequences from genes encoding proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
which are thought to be essential, and to a screening assay for identifying compounds which have a physiological effect on these proteins. Suitable compounds are useful as pesticides and may be in conjunction with other pesticides and herbicides for crop
                                                                                                                                                                                                                                                                                                                                                                           Screening assa
physiological
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nes 18; Conser
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                                                                                                                                                                                                                                                                                                                                                                        assays for used for identifying coical effect on proteins identified
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                           hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases
                                                                                                                   of the breast, fibrocystic non-carcinoma tumours.
                                                                                                                                                                                                                                                                            The present invention relates to novel single exon nucleic ac. The present sequence is one such probe. The probes are useful measuring human gene expression in a human breast sample, when
                                                                      Note: The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                    in a human
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                                                 ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                          SEQ ID No 3879;
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2000US-0234687.
2000US-0236359.
2000US-0024263.
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2000US-0207456.
2000US-0608408.
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Query Match

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RESULY 8
AAI14349/c
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PR 30-JAN
XX O4-FEE
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Matches 16; Conserv
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                                                                                                    expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488901/53.
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26-MAY-2000;
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Local Similarity 100.0%;
les 16; Conservative
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                                                                                        CCCTGATGACCTAATG
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                                                                                                                                                                                                                                                                                        459
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RESULT 10
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XX AAI041
XX O9-OCT
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XX Probe;
KW Probe;
KW Inflam
XX Probe;
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Best Local
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes at for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                               09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn
                                                                                                                     Probe;
                                                                                                                                                            Probe #4170
                                                                                                                                                                                                                                      AAI04179;
                                                                                                                                                                                                                                                                             AAI04179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
26-MAY-2000;
                                                           Homo sapiens.
                                                                                              Probe; human;
inflammatory o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe; microarray; human; placenta; antenatal diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe #4409 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI35723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI35723 standard; DNA; 459
                                                                                                                                                                                                                                                                                                                                                                             409
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16; Conserv
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                                                                                                                                                                                                                                                                             standard; DNA; 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID No 4409;
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                                                                                                                                                          used
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP;
                                                                                                  disease;
                                                                                                                                                                                               (first
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                                                                                                                     breast
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                                                                                                                                                        measure gene expression
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                                                                                              disease; breast cancer; develop
; proliferative breast disease;
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                                                                                                                                                        in human breast sample
                                                                                                                     development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 459;
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                                                                                                  non-carcinoma
                                                                                                                   disorder;
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Best Local S
Matches 16
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
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in a
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         (OHIS ) UNIV OHIO STATE
                                                   19-SEP-1997;
                                                                                                                                         25-MAR-1999
                                                                                                                                                                                    WO9913720-A1
                                                                                                                                                                                                                            Ehrlichia chafeensis
                                                                                                                                                                                                                                                                         detection;
                                                                                                                                                                                                                                                                                                Outer membrane
                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX34755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX34755 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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27-SEP-2000;
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                                                                                            18-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                        encoding
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16; Conser
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2000US-0236359.
2000GB-0024263.
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2000US-0207456.
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                                                   97US-0059353
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Pred. No.
                                                                                                                                                                                                                                                                                              Ehrlichia chafeensis;
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26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 459,
                                                                                                                                                                                                                                                                                              E. canis;
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RESULT 12
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Best Local
                                                                        Assessing cardiovascular status in humans involves comparing polymorphic pattern comprising polymorphic positions within encoding specific proteins, with reference polymorphic pattern
                                                                                                                WPI;
                                                                                                                                                                         14-OCT-1998;
14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. Chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAV06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAV06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                       Disclosure;
                                                                                                                                  Norberg
                                                                                                                                                                                                      13-OCT-1999;
                                                                                                                                                                                                                                           WO200022166-A2
                                                                                                                                                                                                                                                                                         polymorphic marker; cardiovascular disease; myocardial
unstable angina; hypertension; atherosclerosis; stroke
                                                                                                                                                      (EURO-)
                                                                                                                                                                                                                        20-APR-2000
                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                            Angiotensinogen
                                                                                                                                                                                                                                                                                                                               Human
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                                                                                                                                                                                                                                                                                screening;
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                                                                                                                                                                                                                                                                                                                             angiotensinogen (AGT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                      EURONA
                                                                                                                                   ĽĮ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       852
                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rikihisa
                                                     Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                      MEDICAL
                                                                                                                                                                         98US-0104286
98US-0104302
                                                                                                                                                                                                      99WO-IB01678
                                                                                                                                                                                                                                                                                                            gene; AGT; regulatory region; polymorphism;
                                                                                                                                                                                                                                                                                 treatment
                                                                                                                                                                                                                                                                                        hypertension; atherosclerosis; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295
                                                     126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                      563
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                                                                                                                                                      ΑВ
                                                                                                                                   ΜK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .08;
                                                                                                                                                                                                                                                                                 outcome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                              gene regulatory sequence (GenBank X15323).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç;
                                                                                                                                   Lindstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia
                                                                                                                                    PHR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                          pattern
                                                                                                                                                                                                                                                                                        infarction;
prognosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              part
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The invention relates to a novel method of assessing the cardion status in an individual and to newly identified polymorphisms in genes encoding angiotensin-converting enzyme (ACE), angiotensin receptor type 1 (ATI) and type 2 (AT2), angiotensinogen (AGT), is

endothelin receptor

beta-adrenergic

(AGT), renin

the cardiovascular

in

the

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RESULT 13
AAA38324/c
ID AAA383
XX AAA383
AC AAA383
DT 21-AUG
XX
DT 21-AUG
XX
DT 20-AUG
XX
AG Angiot
KW Angiot
KW Angiot
KW Angiot
KW Unstab
KW Unstab
KW Unstab
KW Unstab
XW Uns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C predetermined cardiovascular disease status. The polymorphic markers are cuseful for determining the predisposition of an individual to cardiovascular disorders such as myocardial infarction, unstable angina, chypertension, atherosclerosis and stroke. They are also useful for curiovascular this they cardiovascular status of a patient given a curior treatment regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-curior) and probes for detecting the outcome of a treatment regimen. Creation of the genes comprising a polymorphic site may be used as primers and probes for detecting the outcome of a treatment regimen. Creationary arrays for high throughput screening. The genes, and the proteins creating the variety arrays for high throughput screening. The genes, and the proteins creating a polymorphic pattern reduces or climary arrays for high throughput screening of potential cardiovascular creating a treatment for a particular creating a patient regimen. At the screening of potential cardiovascular creating a treatment for a particular regiment regiment regiment regiments. At a risk for an adverse response, to a particular creatment regiment regiment regiments from clinical trials who are predicted to be correlated with a sub-population of the test population, permitting creating can be approved for use in the adverse results can be evaluated to divide the authority population of the test population, permitting creating can be approved for use in the appropriate population, permitting creating can be approved for use in the appropriate population, permitting creating the number of pattents required for a clinical trial, which in the sequence is not provided and specifical and specifical are 3957/A, 412C/T, 432G/A, Compared for a synthetic sequence is referred to as SBO ID No:122 on page 56 and in the sequence listing. The present sequence is not given in the specific alignment of security sequence is not given in the specific and in the sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                        13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                               Angiotensinogen gene; AGT; coding region; polymorphism; polymorphic marker; cardiovascular disease; myocardial infarction; unstable angina; hypertension; atherosclerosis; stroke; prognosis;
       14-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human angiotensinogen (AGT) gene exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA38324 standard; DNA; 1278
                                                                                                                                             20-APR-2000
                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522 TGGTAAGTTTCACATG 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 tggtaagtttcacatg 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 283 A; 343 C;
       98US-0104286
                                                                        99WO-IB01678
                                                                                                                                                                                                                                                                                                                                                     treatment outcome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      but was obtained from the GenBank database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ν.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 T;
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26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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Z Z X Z Z E

AAQ47075 standard;

DNA; 1491 BP

13-JAN-1994 AAQ47075;

(first entry)

δÃ

Query Match Best Local Matches

16;

Conservative

Similarity

13.0%; out 100.0%; Pr --- 0;

Score 16; Pred. No.

DB 26; 21;

Length 1278; Indels

0;

0

Gaps

0

Sequence 1278

BP;

283

A;

343

Ç 295 G; 357

Τ,

0 other

DЬ

522 TGGTAAGTTTCACATG 71 tggtaagtttcacatg

507 86

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CC Fragments of the genes comprising a polymorphic site may be used as as Clibrary arrays for high throughput screening. The genes, and the proteins CC library arrays for high throughput screening. The genes, and the proteins CC they encode are useful in the screening of potential cardiovascular CC drugs. Determination of an individual's polymorphic pattern reduces or CC eliminates trial and error in selecting a treatment for a particular CC individual cardiovascular patient. It also provides the ability to CC eliminate patients from clinical trials who are predicted to be CC correlated, or at a risk for an adverse response, to a particular CC inon-responsive, or at a risk for an adverse results can be evaluated to identify polymorphic patterns so that the adverse results can be carrelated with a sub-population of the test population, permitting CC exclusion of such sub-population of the test population, thereby decreasing the number of patients required for a clinical trial, which in CC turn decreases the duration and cost of such trials. Sequences A38324 cc A38327 represent exons 2, 3, 4 and 5 of the human angiotensingen gene coding region (GenBank M24686-M24689). The polymorphic sites identified care 273C/T, 620C/T, 893T/C, 912C/T, 997G/C, 11116G/A, 1174C/A; and A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pattern of polymorphisms from the individual with a reference polymorphic pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to cardiovascular disorders such as myocardial infarction, unstable angina, hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a patient given a treatment regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-arenergic receptor antagonists (beta-blockers) or calcium channel blockers). One or more polymorphic markers provides a basis for predicting the outcome of a treatment regimen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptors 1 and 2. The method comprises determining the sequence at one or more polymorphic positions within these genes, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel method of assessing the cardiovascular status in an individual and to newly identified polymorphisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assessing cardiovascular status in humans involves comparing test polymorphic pattern comprising polymorphic positions within genes encoding specific proteins, with reference polymorphic pattern -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes encoding angiotensin-converting enzyme (ACE), angiotensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 111-112; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EURO-) EURONA MEDICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0104302
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antigen

gene

DNA

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RESULT 1
AAC98971/
ID AAC9
XX AAC9
XC AAC9
XX O9-M
XX Huma
KW Huma
KW dete
KW noott
KW anti
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                                                                                                                                                                                                                                                                                                                                                      Matches
Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5. This sequence was isolated by PCR using the primers given in AAQ47068-72. Primer 21B4 | corresponds to part of the repeated region of 21B4/rhoptry antigen. In hybridisation assays this primer recognised two tandemly repeated regions suggesting that B bovis contains two copies of the 21B4/rhoptry antigen gene. The two proteins encoded by the two antigen genes are identical. Primers 21B4.2 and 21B4.3 flank the 21B4-309 cooling region of the antigen gene. Primer 21B4.4 primes synthesis just 3 to the end of the open reading frame. The entire open reading frame was shown to encode five antigen genes. The 3 non-repetitive sequences of open reading frame to the open reading frame. Babesia antigen genes can be used in the production of a combined vaccine which will stimulate a greater immune
                                                                                                                                    09-MAR-2001
                                                                                                   Human pancreatic
                                                                                                                                                                                                  AAC98971 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the Babesia bovis 21B4/rhoptry antigen 5. This sequence was isolated by PCR using the primers given it AAQ47068-72. Primer 21B4.1 corresponds to part of the repeated region of 21B4/rhoptry antigen. In hybridisation assays this part of the repeated region of 21B4/rhoptry antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting closely linked gene copies which encode protective antigen against babesiosis - by screening babesial genomic DN library with oligo-nucleotide probe based partial sequencing protective antigen and identifying positive clones
                                                                                                                                                                     AAC98971;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dalrymple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymerase chain reaction; PCR; amplify; primer; detection; babesiosis; parasite; Babesia bovis; 21B4/rhoptry; antigen; repeat region; immune response; vaccine; ss.
                                                                                                                                                                                                                                                                                   941 cttacaaccctgatga
                                                                                                                                                                                                                                                                                                                   24 cttacaaccctgatga
                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and afford broader immunity than a single antigen vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B₽,
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
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                                                                                                  cancer antigen nucleotide sequence SEQ ID NO:199
                                                                                                                                                                                                                                                                                                                                                                                                                                     479
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                                                                                                                                                                                                                                                                                                                                                                   13.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     286
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     328 G;
                                                                                                                                                                                                                                                                                                                                                                   DB 14;
26;
                                                                                                                                                                                                                                                                                                                                                                                                                                     398 T; 0 other
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AAC78084/c
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AC AAC780
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be us in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used detect, treat or prevent pancreatic disorders, especially cancer agonists and antagonists to the antigens can be screened for. The
                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
                                                                                   08-FEB-2001
                                                                                                                    AAC78084;
                                                                                                                                                      AAC78084 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2732 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins, called pancreatic cancer antigens, given in AAB54008 AAB54466. The human pancreatic cancer antigens have cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC98773 to AAC99231 encode the human pancreatic cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 645-646; 1379pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2000; 2000WO-US05989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200055320-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neural; immune system; muso
pulmonary; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                      TCTTCAATTTATTCCA 1429
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DB; AAB54206.
                                                                                                                                                                                                                                                                                                      Similarity 100
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                        624 A; 753 C;
                                                                                                                                                      CDNA; 4201 BP
                                                                                                                                                                                                                                                                                                 100.0%; --
                                                                                                                                                                                                                                                                                                                                         13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                          exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscular; reproductive; gastrointestinal;
lar; renal; proliferative; ss.
                                                                                                                                                                                                                                                                                                      Score 16; DB Pred. No. 25; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        889
                                                                                                                                                                                                                                                                                                                                                                                        G;
                                                                                                                                                                                                                                                                                                                                                                                                                          of the
                                                                                                                                                                                                                                                                                                                                                                                        659
                                                                                                                                                                                                                                                                                                                      DB
25;
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                                                                                                                                                                                                                                                                                                        0,
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                                                                                                                                                                                                                                                                                                      Gaps
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0

diagnosis;

Human cancer associated gene sequence SEQ ID NO:478.

cer associated gene; cancer
cytostatic; proliferative;

antigen; de vulnerary;

detection;

immunomodulator;

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RESULT 17
AAH33277/c
ID AAH332'
XX
AC AAH332
XX
DT 03-SEP
XX
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                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB4440 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; antiangiogenic; autoimmune disorder; antipsoriatic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
                     03-SEP-2001
                                                           AAH33277;
                                                                                                                                                                                             2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating camellorating medical conditions and diagnosing pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cancer the genes are expressed in Example of activities the genes are expressed in Example of activities
                                                                                              AAH33277 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        include: cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic useful for treating or
                                                                                                                                                                                                                                                                                                                                                                Sequence 4201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                N
                                                                                                                                                                                                                                                                                                                                                                                                    present invention
                                                                                                                                                                                                                              aggtattgtaaatgtg 17
                                                                                                                                                                                           AGGTATTGTAAATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-587533/55
                                                                                                                                                                                                                                                                      L Similarity
16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 1012-1013; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC78448 encode
                                                                                                                                                                                                                                                                      Conservative
                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                BP; 1323 A;
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                                                                                              CDNA; 4201 BP
                                                                                                                                                                                                                                                                                     13.0%;
                                                                                                                                                                                           2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acids comprising sequences encoding peptides
                                                                                                                                                                                                                                                                                                                                                                637
                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                     Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                              C; 850
                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                              G; 1381 T; 10 other;
                                                                                                                                                                                                                                                                                   DB
25;
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                                                                                                                                                                                                                                                                                                     Length 4201;
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                                                                                                                                                                                                                                                                  Gaps
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RESULT 1 AAC91600/

AAC91600 standard; DNA; 5308

ВP

₽ δÃ

2555

N

aggtattgtaaatgtg 17 AGGTATTGTAAATGTG 2540

Query Match Best Local Matches

16;

Conservative

0,

Mismatches

0;

Indels

0;

Gaps

0,

Similarity

13.0%;

Score 16; Pred. No.

25;

22;

Length 4201;

Sequence 4201 BP; 1323 A; 637 C;

850 G; 1381

;

10 other

16-MAR-2001 AAC91600

(first

entry)

Human angiotensinogen gene; AGT; insulin-dependent diabetes mellitus; type 1 diabetes; chromosome 1q42-43; single nucleotide polymorphism; IDDM; SNP; diagnosis; susceptibility; transgenic animal; drug screening;

Human angiotensinogen gene 5' region/exon 1, SEQ ID NO:1.

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the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                        present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                         AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human cancer-associated nucleic acid molecules (N) and proteins (P).
                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colorectal carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon cancer antigen encoding cDNA SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-235357/24
                                                                                                                                                                                                                                                                                                                                                                                                1; Page 2445-2447; 9803pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US26524
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99US-0163280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CE,
                                                                                                                                                                                                                                                                                                                                                                                                English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA;
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                                                                                                                                                                                                                                                                                                                                           colon, where
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X A X A X B
                                                                                                AAC91670,
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                                                                                                                                                                                                                                                                                                                    RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                              CC claimed human AGT mutant nucleic acid sequences AAGJ1667-C91684, and the cumutant angiotensinogen proteins ABA8945-B84949. The invention also createst to detecting mutant AGT alleles or gene products thereof which CC are related to IDDM; determining whether a person has, or is at risk of CC developing diabetes via detection of a polymorphism in the AGT gene; and CC methods of screening for drug candidates which may be useful in the CC treatment of diabetes resulting from an AGT mutation. Methods of CC preventing or treating diabetes are claimed which comprise the CC administration of a compound which agonises or antagonises wild-type or CC mutant AGT, which agonises or antagonises an AGT receptor, which adonises or antagonises AGT proteins. In addition, CC inhibits AGT gene expression, or which cleaves AGT proteins. In addition, CC inhibits AGT gene expression a mutant human AGT allele. The CC person has, or is at risk from developing insulin-dependent diabetes. Mutant CC AGT proteins or fragments thereof are useful for screening compounds of which hind to AGT molument these The present segments contents.
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutant alleles of which cause a susceptibility to insulin-dependent diabetes mellitus (IDDM, type I diabetes). The AGT gene is located on chromosome 1942-43, a region linked to IDDM. The invention discloses genomic sequences comprising exons 1-5 of the human AGT gene (AAC91600-C91604) and a genomic sequence comprising an alternative AGT gene exon 1 (AAC91606). The invention also encompasses the specifically claimed human AGT mutant nucleic acid sequences AAC91667-C91684, and the
                                                                                                                                                                   2311
                 16-MAR-2001
                                                 AAC91670;
                                                                                AAC91670 standard;
                                                                                                                                                                                                                                                                                                                    Sequence 5308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the human angiotensinogen (AGT) gene, some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin-dependent diabetes mellitus useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY-1999; 99US-0135423
06-JAN-2000; 2000US-0174700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antidiabetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-2000; 2000WO-US13327
                                                                                                                                                                                                 71 tggtaagtttcacatg 86
                                                                                                                                                                                                                                                  Local
                                                                                                                                                               TGGTAAGTTTCACATG 2296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-025172/03
                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                Similarity 100
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                       of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of predisposition
                                                                                                                                                                                                                                                                                                                                                                to AGT polypeptides. The present sequence represents {\bf f} the human AGT gene comprising part of the 5' region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Russell DL,
              (first entry)
                                                                                                                                                                                                                                                                                                                    BP; 1364 A; 1265 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60-63;
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                                                                                DNA; 5308 BP
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                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83pp; English.
                                                                                                                                                                                                                                                                   13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shattuck DM;
                                                                                                                                                                                                                                                Score 16;
Pred. No.
                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5' region; exon
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                    1329 G; 1350 T;
                                                                                                                                                                                                                                              DB
25;
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                                                                                                                                                                                                                                                                                                                                                                      exon
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Query Match
Best Local S
                                                                                                                                                                                inhibits AGT gene expression, or which cleaves AGT proteins. In addition, the invention encompasses a transgenic non-human animal, or cell line derived therefrom, comprising a mutant human AGT allele. The polymorphisms identified in the AGT gene are useful for determining if a person has, or is at risk from developing insulin-dependent diabetes mellitus. AGT modulators can be used to treat or prevent diabetes. Mutant AGT proteins or fragments thereof are useful for screening compounds which bind to AGT polypeptides. The present sequence represents a portion of the human AGT gene comprising a mutant 5' region fragment, and exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the human angiotensinogen (AGT) gene, some mutant alleles of which cause a susceptibility to insulin-dependent diabetes mellitus (IDDM, type I diabetes). The AGT gene is located on chromosome 1q42-43, a region linked to IDDM. The invention discloses genomic sequences comprising exons 1-5 of the human AGT gene (AAC91600-C91604) and a genomic sequence comprising an alternative AGT gene exon 1 (AAC91606). The invention also encompasses the specifically claimed human AGT mutant nucleic acid sequences AAC91667-C91884, and the mutant angiotensinogen proteins AAB48945-B48949. The invention also relates to detecting mutant AGT alleles or gene products thereof which are related to IDDM; determining whether a person has, or is at risk of developing diabetes via detection of a polymorphism in the AGT gene; and methods of screening for drug candidates which may be useful in the
                                                                                                                                                                                                                                                                                                                                                                            treatment of diabetes resulting from an AGT mutation. Methods of preventing or treating diabetes are claimed which comprise the administration of a compound which agonises or antagonises wild-type or mutant AGT, which agonises or antagonises an AGT receptor, which
                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page -; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin dependent diabetes mellitus usefi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type 1 diabetes; chromosome 1942-43; single nucleotide polymorphism; IDDM; SNP; diagnosis; susceptibility; transgenic animal; drug screenir antidiabetic; gene therapy; 5' region; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis of predisposition to diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McGrail M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-1999; 99US-0135423
06-JAN-2000; 2000US-0174700
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                                                                                                                           : The present sequence is not shown in the specification, but is
from the wild-type human AGT gene 5' region/exon 1 sequence
n page 60-63.
                                                                                    5308 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Russell DL,
                                                                                    1364
  13.0%;
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                                                                                  A; 1264 C; 1329 G; 1351 T; 0 other,
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  Score 16;
Pred. No.
  25,
                     22;
                     Length 5308;
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Matches

16;

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Mismatches

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Gaps

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Similarity

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AAC91671/c

ID AAC91671;

XC AAC91671;

XX AAC91671;

XX Human angiotensinogen general sequence of the human angiotensinogen general sequence composition of a 
                                                                                                      c mutant alleles of which cause a susceptibility to insulin-dependent con chromosome 1942-43, a region linked to IDDM. The AGT gene is located con chromosome 1942-43, a region linked to IDDM. The invention conclusions genomic sequences comprising exons 1-5 of the human AGT gene concluses genomic sequence comprising exons 1-5 of the human AGT gene conclusions of the invention also encompasses the specifically claimed human AGT mutant nucleic acid sequences AAC91607-C91684, and the cutant angiotensinogen proteins AAB48945-B48949. The invention also relates to detecting mutant AGT alleles or gene products thereof which care relates to detecting mutant AGT alleles or gene products thereof which conclusions of screening for drug candidates which may be useful in the treatment of diabetes resulting from an AGT mutation. Methods of companies of a polymorphism in the AGT gene; and treatment of diabetes are claimed which may be useful in the cutant AGT, which agonises or antagonises or antagonises wild-type or mutant AGT, which agonises or antagonises wild-type or cutant AGT, which agonises or antagonises wild-type or cutant AGT, which agonises or antagonises wild-type or cutant AGT mecompasses a transgenic non-human animal, or cell line cutant in the AGT gene are useful for determining if a person has, or is at risk from developing insulin-dependent diabetes. Mutant AGT proteins or fragments thereof are useful for screening compounds which bind to AGT gene comprising a mutant 5' region fragment, and exon constitution of the human AGT gene comprising a mutant 5' region fragment, and exon constitution of the wild-type human AGT gene 5' region fragment, and exon constitution of the wild-type human AGT gene 5' region fragment, and exon constitution of the wild-type human AGT gene 5' region fragment, and exon constitution of the wild-type human AGT gene 5' region fragment, and exon constitution of the wild-type human AGT gene 5' region fragment and constitution of the middle fragment and fragment and constitution of the fra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the human angiotensinogen (AGT) gene, some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page -; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis of predisposition to diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin-dependent diabetes mellitus useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAY-1999; 99US-0135423.
06-JAN-2000; 2000US-0174700.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-2001 (first entry)
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            5308 BP; 1364 A; 1266 C;
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            1329
        G; 1349
            T; 0 other
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Matches Query Match Best

Local Similarity 100 hes 16; Conservative

13.0%; Sur 100.0%; Pr

Score 16; Pred. No.

DB 25; 22; 0,

Length 5308; Indels

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Gaps

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Mismatches

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                                                                                                                                                                                                                                                                                                            mutant alleles of which cause a susceptibility to Insulin dependent characteristics of which cause a susceptibility to Insulin dependent diabetes mellitus (IDDM, type 1 diabetes). The AGT gene is located on chromosome 142-43, a region linked to IDDM. The invention discloses genomic sequences comprising exons 1-5 of the human AGT gene (AAC91600-C91604) and a genomic sequence comprising an alternative AGT gene exon 1 (AAC91606). The invention also encompasses the specifically claimed human AGT mutant nucleic acid sequences AAC91667-C91684, and the mutant angiotensinogen proteins AAB48945-B48949. The invention also mutant angiotensinogen proteins AAB48945-B48949. The invention also relates to detecting mutant AGT alleles or gene products thereof which are related to IDDM; determining whether a person has, or is at risk of developing diabetes via detection of a polymorphism in the AGT gene; and methods of screening for drug candidates which may be useful in the treatment of diabetes resulting from an AGT mutation. Methods of preventing or treating diabetes are claimed which comprise the
              person has, or is at risk from developing insulin-dependent diabetes mellitus. AGT modulators can be used to treat or prevent diabetes. Mutant AGT proteins or fragments thereof are useful for screening compounds which bind to AGT polypeptides. The present sequence represents a portion of the human AGT gene comprising a mutant 5' region fragment, and exon 1. Note: The present sequence is not shown in the specification, but is derived from the wild-type human AGT gene 5' region/exon 1 sequence
                                                                                                                                                                          administration of a compound which agonises or antagonises wild-type or mutant AGT, which agonises or antagonises an AGT receptor, which inhibits AGT gene expression, or which cleaves AGT proteins. In addition, the invention encompasses a transgenic non-human animal, or cell line derived therefrom, comprising a mutant human AGT allele. The polymorphisms identified in the AGT gene are useful for determining if a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin-dependent diabetes mellitus useful for diagnosis of predisposition to diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human angiotensinogen gene; AGT; insulin-dependent diabetes mellitus; type 1 diabetes; chromosome 142-43; single nucleotide polymorphism; IDDM; SNP; diagnosis; susceptibility; transgenic animal; drug screeni antidiabetic; gene therapy; 5' region; mutant; exon 1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the human angiotensinogen (AGT) gene, some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page -; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McGrail M, Russell DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MYRI-) MYRIAD GENETICS
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06-JAN-2000;
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Sox

Sequence 5308 BP; 1364 A; 1264 C; 1329 G; 1351 T;

0 other;

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RESULT 22
AAC91674/c
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The invention relates to the human angiotensinogen (AGT) gene, some CC mutant alleles of which cause a susceptibility to insulin dependent CC diabetes mellitus (IDDM, type 1 diabetes). The AGT gene is located CC on chromosome 1942-43, a region linked to IDDM. The invention CC discloses genomic sequences comprising exons 1-5 of the human AGT gene CC (AAC91600-C91604) and a genomic sequence comprising an alternative AGT CC gene exon 1 (AAC91606). The invention also encompasses the specifically CC claimed human AGT mutant nucleic acid sequences AAC91667-C91684, and the CC mutant angiotensinogen proteins AAB48945-B48949. The invention also CC relates to detecting mutant AGT alleles or gene products thereof which CC are related to IDDM; determining whether a person has, or is at risk of CC developing diabetes via detection of a polymorphism in the AGT gene; and CC methods of screening for drug candidates which may be useful in the CC preventing or treating diabetes are claimed which comprise the CC administration of a compound which agonises or antagonises wild-type or mutant AGT, which agonises or antagonises an AGT receptor, which comprisms identified in the AGT gene as AGT proteins. In addition, the invention encompasses a transgenic non-human animal, or cell line CC polymorphisms identified in the AGT gene are useful for determining if a polymorphisms identified in the AGT gene are useful for determining if a person has, or is at risk from developing insulin-dependent diabetes
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06-JAN-2000; 2000US-0174700
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                                                                                                                                                                                                                                                                                                                                                                                                                               of predisposition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Russell DL,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetes
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25;
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RESULT 2
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ID AAC9
XX AAC9
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XX Huma
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Best Local
                                                                     discloses genomic sequences comprising exons 1-5 of the human AGT gene (AAC91600-C91604) and a genomic sequence comprising an alternative AGT gene exon 1 (AAC91606). The invention also encompasses the specifically claimed human AGT mutant nucleic acid sequences AAC91667-C91684, and the mutant angiotensinogen proteins AAB48945-B48949. The invention also relates to detecting mutant AGT alleles or gene products thereof which are related to IDDM; determining whether a person has, or is at risk of developing diabetes via detection of a polymorphism in the AGT gene; and methods of screening for drug candidates which may be useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                        mutant alleles of which cause a susceptibility to insulin-dependent diabetes mellitus (IDDM, type 1 diabetes). The AGT gene is located on chromosome 1q42-43, a region linked to IDDM. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin-dependent diabetes mellitus usefi diagnosis of predisposition to diabetes -
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|||||||||||||||
2311 TGGTAAGTTTCACATG 2296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human angiotensinogen gene; AGT; insulin-dependent diabetes mellitus; type I diabetes; chromosome 1424-43; single nucleotide polymorphism; IDDM, SNP, diagnosis; susceptibility; transgenic animal; drug screeniantidiabetic; gene therapy; 5' region; mutant; exon 1; ds.
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06-JAN-2000; 2000US-0174700
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        treatment of diabetes resulting 
preventing or treating diabetes
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Pred. No.
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The invention relates to the human angiotensinogen (AGT) gene, some mutant alleles of which cause a susceptibility to insulin-dependent diabetes mellitus (IDDM, type 1 diabetes). The AGT gene is located on chromosome 1q42-43, a region linked to IDDM. The invention discloses genomic sequences comprising exons 1-5 of the human AGT gene (AAC91600-C91604) and a genomic sequence comprising an alternative AGT gene exon 1 (AAC91606). The invention also encompasses the specifically claimed human AGT mutant nucleic acid sequences AAC91667-C91684, and the
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Pred. No.
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DT 16-M
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Huma
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KW Huma
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KW HUMA
KW AITLI
OS HOMO
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Best Local
                                                                                                              Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin-dependent diabetes mellitus useful diagnosis of predisposition to diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1677/c
AAC91677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             person has, or is at risk from developing insulin-dependent diabetes mellitus. AGT modulators can be used to treat or prevent diabetes. Mutant AGT proteins or fragments thereof are useful for screening compounds which bind to AGT polypeptides. The present sequence represents a portion of the human AGT gene comprising a mutant 5' region fragment, and exon 1. Note: The present sequence is not shown in the specification, but is derived from the wild-type human AGT gene 5' region/exon 1 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant AGT, which agonises or antagonises an AGT receptor, which inhibits AGT gene expression, or which cleaves AGT proteins. In addition, the invention encompasses a transgenic non-human animal, or cell line derived therefrom, comprising a mutant human AGT allele. The polymorphisms identified in the AGT gene are useful for determining if a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relates to detecting mutant AGT alleles or gene products thereof which are related to IDDM; determining whether a person has, or is at risk of developing diabetes via detection of a polymorphism in the AGT gene; and methods of screening for drug candidates which may be useful in the treatment of diabetes resulting from an AGT mutation. Methods of preventing or treating diabetes are claimed which comprise the administration of a compound which agonises or antagonises wild-type or
                                                          Claim 2; Page -; 83pp;
                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-1999;
06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDDM; SNP; diagnosis; susceptibility; transgenic ani antidiabetic; gene therapy; 5' region; mutant; exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human angiotensinogen gene; AGT; insulin-dependent diabetes mellitus; type 1 diabetes; chromosome 1q42-43; single nucleotide polymorphism; IDDM; SNP; diagnosis; susceptibility; transgenic animal; drug screeni
                                                                                                                                                                                                                                                                                                McGrail M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-2000; 2000WO-US13327
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                                                                                                                                                                                                                                                                                                                                                          (MYRI-) MYRIAD GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200071751-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human angiotensinogen gene 5' region mutant, G2829A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC91677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5308 BP; 1364 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       snown on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 tggtaagtttcacatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    page 60-63.
                                                                                                                                                                                                                                                                                                Russell DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0135423
2000US-0174700
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                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5308
                                                                                                                                                                                                                                                                                                Shattuck DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1266 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 5308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug screening;
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The invention relates to the human angiotensinogen (AGT) gene,

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RESULT 26
AAX23517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC diabetes mellitus (IDDM, type 1 diabetes). The AGT gene is located CC on chromosome 1q42-43, a region linked to IDDM. The invention CC discloses genomic sequences comprising exons 1-5 of the human AGT gene CC (AAC91600-091604) and a genomic sequence comprising an alternative AGT CC gene exon 1 (AAC91606). The invention also encompasses the specifically CC claimed human AGT mutant nucleic acid sequences AAC91607-091604 and the CC creates to detecting mutant AGT alleles or gene products thereof which CC are related to IDDM, determining whether a person has, or is at risk of CC methods of screening for drug candidates which may be useful in the CC methods of screening for drug candidates which may be useful in the CC mutant AGT, which agonises or antagonises or antagonises wild-type or CC mutant AGT, which agonises or antagonises wild-type or CC mutant AGT, which agonises or antagonises wild-type or CC mutant AGT, which agonises or antagonises an AGT proteins. In addition, the invention encompasses a transgenic non-human animal, or cell line CC the invention encompasses a transgenic non-human animal, or cell line CC polymorphisms identified in the AGT gene are useful for determining if a CC mellitus. AGT modulators can be used to treat or prevent diabetes Mutant CC which bind to AGT polypeptides. The present sequence represents a portion cof the human AGT gene comprising a mutant buman AGT manuer. AGC compounds of a compounds of actived from the wild-type human AGT gene is not shown in the specification, but is CC derived from the wild-type human AGT gene 5' region/exon 1 sequence CC shown on page 60-63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                               WPI; 1999-205193/17
                                                                                                 (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.
                                                                                                                                    02-SEP-1997;
                                                                                                                                                                   02-SEP-1998;
                                                                                                                                                                                                    11-MAR-1999
                                                                                                                                                                                                                                    W09911799-A2
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                      proteinaceous
                                                                                                                                                                                                                                                                                                                       arterial
                                                                                                                                                                                                                                                                                                                                  Aminopeptidase; human; AmP; gene therapy; treatment; AmP-deficiency; prenatal diagnosis; angioedema; antihypertensive agent; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                    Human kidney
                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2311 TGGTAAGTTTCACATG 2296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 tggtaagtttcacatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                       stenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             page 60-63.
                                                              Sprinkle TJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                    aminopeptidase P genomic DNA fragment 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                      waste
                                                                                                                                  97US-0057854
                                                                                                                                                                   98WO-US18426
                                                                                                                                                                                                                                                                                                      degradation;
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                                                              Venema
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
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Pred. No.
                                                                RC
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25;
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                                                                                                                                                                                                                                                                                                    immunohistochemistry; ss
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Nucleic

acid

encoding

human

aminopeptidase

Example 2;

Page 33; 83pp; English

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                                              Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin-dependent diabetes mellitus useful for diagnosis of predisposition to diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             also used to identify Amp-expressing sequences in other animals and to generate transgenic animals, and comparisons of genomic sequences are used to detect mutations. Amp inhibitors are potentially useful as antihypertensive agents and to prevent or treat arterial (re)stenosis or atherosclerosis. The structure of Amp is used to design synthetic substrates, e.g. for use in Amp assays. Amp, which hydrolyzes N-terminal imido bonds, can be used to degrade industrial protein feeds to free
                                                                                                                                                 McGrail M,
                                                                                                                                                                                                                                                                                                                                                                                               Human angiotensinogen gene; AGT; insulin-dependent diabetes mellitus; type 1 diabetes; chromosome 1942-43; single nucleotide polymorphism; IDDM; SNP, diagnosis; susceptibility; transgenic animal; drug screeni antidiabetic; gene therapy; 5' region; promoter; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acids, to degrade proteinaceous wastes, as additives in enzyme formulations used to treat malabsorption syndrome and for studying its biological role. Antibodies against Amp are used in immunohistochemical methods to study Amp distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heterozygous Amp deficiency, including prenatal diagnosis (patients defective in Amp are at risk of developing angloedema if treated with anglotensin-converting enzyme inhibitors), also as antisense inhibitors in cases of excessive Amp expression. The product of the invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for gene therapy for treating AmP-deficiency conditions. Its fragments are used as primers and probes to identify patients with homozygous an
                                                                                                                                                                                                                  06-JAN-2000; 2000US-0174700
                                                                                                                                                                                                                                   21-MAY-1999;
                                                                                                                                                                                                                                                                  16-MAY-2000; 2000WO-US13327.
                                                                                                                                                                                                                                                                                                    30-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC91627 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50000 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes the isolation of a novel human aminopeptidase P (AmP). This protein is used to produce recombinant AmP and can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC91627;
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                                                                                                                                                                                (MYRI-) MYRIAD GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 acaaccctgatgacct 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiotensinogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                 Russell DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                   Shattuck DM
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic PCR primer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24
24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12846 T; 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 50000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO:29
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0

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RESULT
AAV7285
ID AAV
XX AA
XX AA
XX AA
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XX AA
AC
AB
XX AA
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC The invention relates to the human angiotensinogen (AGT) gene, some CC mutant alleles of which cause a susceptibility to insulin-dependent CC diabetes mellitus (IDDM, type 1 diabetes). The AGT gene is located CC on chromosome 142-43, a region linked to IDDM. The invention CC (AAC91600-C91604) and a genomic sequence comprising an alternative AGT Gene exon 1 (AAC91605). The invention also encompasses the specifically CC claimed human AGT mutant nucleic acid sequences AAC91667-C91684, and the CC mutant angiotensinogen proteins AAB48945-B48949. The invention also contained the CC are related to IDDM; determining whether a person has, or is at risk of CC are related to IDDM; determining whether a person has, or is at risk of CC methods of screening for drug candidates which may be useful in the CC methods of screening for drug candidates which may be useful in the CC mutant AGT, which agonises or antagonises or antagonises wild-type or CC mutant AGT, which agonises or antagonises an AGT receptor, which CC inhibits AGT gene expression, or which cleaves AGT proteins. In addition, the invention encompasses a transgenic non-human animal, or cell line CC derived thereform, comprising a mutant human AGT allele. The CC methods of screening compounds in the AGT gene are useful for determining if a person has, or is at risk from developing insulin-dependent diabetes. Mutant CC AGT proteins or fragments thereof are useful for screening compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; tryptophan 2,3-dioxygenase; TDO2; allelic polygene diagnosis; reward deficiency syndrome; RDS; obesity; alcohol; tobacco; drug use; Tourette syndrome; attention deficit hyperactivity disorder; ADHD; schizoid/avoidant behaviour; aggression; premenstrual syndrome; violence; hostility; mania; depression; anxiety; sleep problem; autism; osteoporosis; binge eating; craving; inhibition; PCR primer; ss.
                                                                                          (BLUM-)
                                                            (TEXA
                                                                                                                                                                               29-APR-1997;
                                                                                                                                                                                                                                      29-APR-1998;
                                                                                                                                                                                                                                                                                            05-NOV-1998
                                                                                                                                                                                                                                                                                                                                                      WO9848785-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tryptophan 2,3-dioxygenase oligonucleotide variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV72858 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGT proteins or fragments thereof are useful for screening compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 ggtaagtttcacatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTAAGTTTCACATG
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15; Conserv
                                                            BLUM
CITY
UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to AGT polypeptides. The present sequence represents a region/promoter PCR primer used in an exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                      INC KENNETH.
OF HOPE NAT MEDICAL
TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                         97US-0044394.
                                                                                                                                                                                                                                      98WO-US08684.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Sequence

96

BP;

38

A; 7 C;

20 G;

31 T; 0 other;

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include: substance use disorders; obesity; alcohol, tobacco or other drug use; Tourette syndrome; attention deficit hyperactivity disorder (ADHD); schizoid/avoidant behaviour; aggression; premenstrual syndrome; violence; hostility; mania; depression; anxiety; sleep problems, autism Methods given in the invention can be applied for diagnosis of RDS or e.g. elevated levels of low density lipoprotein (LDD) or cholesterol, longevity, lack of ADHD, osteoporosis. In treatment of obesity, (A) inhibits binge eating and craving. The present sequence represents an oligonucleotide used in an example from the present invention.
                                                                                                                                                                                                                                                                           deficiency syndrome (RDS) behaviour; or (ii) preventing or treating unwanted weight gain. (A) comprises: (a) an agent (I), i.e. amino acid or peptide, or their analogues or derivatives, that inhibits enzymatic destruction of a neuropeptidyl opiate; (b) a neurotransmitter precursor (II) to promote neurotransmitter synthesis, i.e. L-Tyr, L-Phe or L-dopa (dopamine precursors) L-Trp or 5-hydroxytryptophan (serotonin precursors) or L-Glu (or its sait) or L-Gln (gamma-aminobutyric acid precursors); and (c) chromium picolinate or nicotinate to increase the level of Trp. Typical of many behaviours that can be treated with (A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition for treating reward deficiency syndrome behaviour, attention deficit disorders or controlling weight - contains inhibitor of opiate peptide destruction, neurotransmitter prec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Page 293; 663pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A composition (A) has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1998-610008/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   been developed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurotransmitter precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (i) treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a reward
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RESULT 3
AAC65347
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Best Local :
                                                                                                                                        post-traumatic stress syndrome; pre-menstrual syndrome; cannabinoid receptor gene; dopamine DRD4 receptor; tryptophan 2,3-dioxygenase; TDO2; PCR primer; ss.
                                                                                                                                                                     neurotransmitter synthesis promoter; tryptophan-concentration enhancing; allelic polygene diagnosis; reward deficiency syndrome; RDS; obesity; smoking; Tourette's syndrome; schizoid avoidant behaviour; aggression;
                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                    AAC65347 standard; DNA; 96
        (CITY ) CITY OF HOPE NAT MEDICAL CENT. (TEXA ) UNIV TEXAS SYSTEM.
                                       29-APR-1998;
                                                          29-APR-1998;
                                                                              17-OCT-2000
                                                                                                  US6132724-A
                                                                                                                                                                                                                                           12-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                         29
                                                                                                                                                                                                                                                                                                                                    TDO2
                                                                                                                                                                                                    anti-ADD;
                                                                                                                                                                                                                                                                                                                                                                                Similarity
15; Conser
                                                                                                                                                                                                                       gene G to T variant oligomer #1.
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                       980S-0069886
                                                          9886900-8086
                                                                                                                                                                                                    anti-ADHD; opiate destruction inhibitor;
                                                                                                                                                                                                                                                                                                                                                                           12.2%; 500
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                       29
                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                     15;
No.
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94
                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 96
                                                                                                                                                                                                                                                                                                                                                                                Indels
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Blum K,

Comings DE,

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HAV7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                              2819
                                                                                 (BLUM-)
(CITY )
(TEXA )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis of reward deficiency syndrome. Compositions are disclosed which comprise at least one substance that inhibits the enzymatic destruction of a neuropeptidyl opiate, at least one neurotransmitter, a tryptophan concentration-enhancing amount of a mineral compound; and at least one substance chosen from Rhodiola extract and huperzine. The compositions are used to treat ADD and ADHD. They are used to treat reward deficiency syndrome (RDS) behaviours including obesity, smoking, Tourette's syndrome, pre-menstrual syndrome or tobacco use. The presence of enkephalin releasers dramatically improves the patient's response to
  attention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
                                    WPI; 1998-610008/51.
                                                            Blum
                                                                                                                                                                                  05-NOV-1998
                                                                                                                                                                                                          WO9848785-A2
                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                      Tourette syndrome; attention deficit hyperactivity disorder; Auschizoid/avoidant behaviour; aggression; premenstrual syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                        AAV72819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compositions used to treat attention deficit (hyperactivity) disorder have of neuropeptidyl opiate enzymatic destruction inhibitor, neurotransmitter, mineral compound and Rhodiola extract or huperzine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blum
                                                                                                                                   29-APR-1997;
                                                                                                                                                          29-APR-1998;
                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                      osteoporosis;
                                                                                                                                                                                                                                                                                  violence;
                                                                                                                                                                                                                                                                                                    Human; tryptophan 2,3-dioxygenase; TDO2; allelic polygene diagnosis; reward deficiency syndrome; RDS; obesity; alcohol; tobacco; drug use Tourette syndrome; attention deficit hyperactivity disorder; ADHD;
                                                                                                                                                                                                                                                                                                                                                         Tryptophan 2,3-dioxygenase
                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                               AAV72819 standard; DNA; 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
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15; Conser
                                                                                  BLUM
CITY
UNIV
                                                           Comings DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
on for treating reward deficiency deficit disorders or controlling
                                                                                                                                                                                                                                                                                hostility; mania;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Column 169;
                                                                                 INC KENNETH.
OF HOPE NAT MEDICAL
TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                    binge eating;
                                                                                                                                   97US-0044394
                                                                                                                                                          98WO-US08684
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                                                          Ιvy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207pp; English.
                                                                                                                                                                                                                                                                                                                                                        oligonucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                    craving; inhibition;
                                                                                                                                                                                                                                                                                depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ე.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 T;
                                                                                              CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
                                                                                                                                                                                                                                                                                 anxiety;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for the allelic polygene
syndrome
weight -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                   PCR primer; ss
                                                                                                                                                                                                                                                                                sleep problem; autism;
                                                                                                                                                                                                                                                                                                                                                        NO:27
behaviour contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disclosed which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                   use;
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                                                                                                                                                                                                                                                                                            RESULT
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Best Local S
Matches 15
                                                                                                                                                                                neurotransmitter synthesis promoter; tryptophan-concentration enhancing; allelic polygene diagnosis; reward deficiency syndrome; RDS; obesity; smoking; Tourette's syndrome; schizoid avoidant behaviour; aggression;
                                               (CITY )
                                                                        29-APR-1998;
                                                                                                         17-OCT-2000
                                                                                                                         US6132724-A
                                                                                                                                                        post-traumatic stress syndrome; pre-menstrual syndrome; cannabinoid receptor gene; dopamine DRD4 receptor; tryptophan 2,3-dioxygenase; TDO2; PCR primer; ss.
                                                                                        29-APR-1998;
                                                                                                                                         Homo sapiens
                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                          Human TDO2 gene G to T variant oligomer #4.
                                                                                                                                                                                                                                           12-FEB-2001
                                                                                                                                                                                                                                                           AAC65362;
                                                                                                                                                                                                                                                                           AAC65362 standard;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            deficiency syndrome (RDS) behaviour; or (ii) preventing or treating unwanted weight gain. (A) comprises: (a) an agent (I), i.e. amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor of opiate peptide destruction, and chromium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A composition (A) has been developed for: (i) treating a reward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 19; Page 398; 663pp; English
                                                                                                                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                                                                           31
                                                                                                                                                                                                                                                                                                                           ggtattgtaaatgtg
                                                                                                                                                                                                                                                                                                                  ggtattgtaaatgtg
                                                                                                                                                                                                          anti-ADD; anti-ADHD; opiate destruction inhibitor;
                                                CITY
                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                               II 12.2%;
Similarity 100.0%;
15; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                            101
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94;
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Compositions used

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treat attention

deficit (hyperactivity) disorder

WPI; 2000-678662/66.

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RESULT 3
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AAZ36299
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis of reward deficiency syndrome. Compositions are disclosed which comprise at least one substance that inhibits the enzymatic destruction of a neuropeptidyl opiate, at least one neurotransmitter, a tryptophan concentration-enhancing amount of a mineral compound; and at least one substance chosen from Rhodiola extract and huperzine. The compositions are used to treat ADD and ADHD. They are used to treat reward deficiency syndrome, schizoid avoidant behaviour, aggression, post-traumatic stress syndrome, pre-menstrual syndrome or tobacco use. The presence of enkephalin releasers dramatically improves the patient's response to treatment.
AAZ36290-Z36320 represent genes or expressed sequence tags (ESTs) identified by the method of the invention. The sequences were isolated from rat osteoblasts. The specification describes a method for the identification of genes responsive to a specific mechanical stress. The method comprises applying the mechanical stress to an organism (tissue or cells comprising bone cells), isolating the specific cellular fractions and extracting mRNA from them, and differentially analysing the mRNA in comparison with control samples. The method is used to identify genes whose expression is responsive to a specific stress. The identifications are control to the specific stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed sequence osteoporosis; bone
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                                                                                                                                                                                                                                                                              (QUAR-) QUARK
                                                                                                                                                                                                                                                                                                          15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                    14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mechanical stress induced glutamyl-cystein synthetase
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density; bone development; ss.
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                                                                                                                                                                         s induced genes for determining controlling osteoporosis -
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Best Local
                                                                    The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes are employed in determining risk associated with a physiological or disease state. The risk determination methods are used for testing a medicament for gene therapy. These medicaments, or genes identified by the method of the invention, are used for treating, preventing or controlling a physiological or disease state (especially osteoporosis or bone density or other factors causing or contributing to osteoporosis or its symptoms or other conditions involved in mechanical stress or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 17330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and diagnostic, forensic, gene therapy and chromosome mapping prodising the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
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        The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                            genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
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15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
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                                                                                                                                                                                                                          AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed
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negative
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HYSEQ I
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                                                                                                                                                                                                                                                                                                                                                                                                            d C, Giese K,
3, Drmanac R,
itz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                              Page
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98US-0085537.
98US-0085696.
98US-0105234.
                                                                                                                                                                                                                                                                                                                                              library used to
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ptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105877
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100.0%;
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Randazzo F, Ke
Crkvenjakov R,
Garcia V, Jon
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Pred. No.
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R, Dickson M,
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inac S, I
rain B;
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PR 24-FEI
PR 03-API
PR 28-JAN
PR 24-FEI
PR 03-API
XX O13-API
PR 28-JAN
PR 24-FEI
PR 11-ESCOM
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Matches
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Lamson G, Le
Stache-Crain
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28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
03-APR-1998;
                  polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polynucrphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to
                                                                                                                                                                                                                             differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779.
                                                                                                                                                                                                                                                                                                 The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human genes and their differentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crkvenjakov R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-1999
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detection; m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-)
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HYSEQ I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kassam A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
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rcia PD, Garcia V, Giese K,
am A, Kennedy GC, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US01619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g; tissue typing; profiling; forensic; cancer;
colorectal cancer; breast cancer; lung cancer;
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D, Pot D, Randazzo F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100
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                                                                            sequences from the Coryneform bacterium Corynebacterium glitamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria ere useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-APR-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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Senoh A, Ik
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da M, Ozaki A;
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Best Local S
Matches 15
                         AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antithflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiparkint; immunosuppressant; cardiant immunosupment, thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiparking antiparkin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 916; 5507pp; English.
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Pred. No.
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RESULT 38
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              human secreted proteins expressed in prostate, and encode the proteins given in AAY11716 to AAY11933 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                    New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematop
                                                                                                                                                                                                                                                                                                                                                                           Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vectors. The proteins and nucleic acids may be used to treat cano proliferative disorders, neurodegenerative disorders, osteoarthrigraft vs host disease, cardiovascular disease, disease mellitus,
                                                                                                                                                                                                                                                    regulating, anti-inflammatory
                                                                                                                                                                                                                                                                                                                          P-PSDB;
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                                                                                                                                                                                                                 Page 453;
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                                                                                                                                                                                                               675pp; English.
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91;
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                                                                                                                                                                                                                                                                   haematopoiesis
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                       of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also use in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                        sequences usually correspond mainly to the 3' untranslated region (UTR)
                                                                                                                                                   The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                           diagnostic,
                                                                                                                                                                                                                                                        obtaining cDNAs and
                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards
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mapping;
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to 5'ESTs and for
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                                                                                                                                                                                                                                                            The present sequence is one of 3351 sequences in a library of human complete the polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes con antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia,
                                                                          Matches
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams LT, Escobedo J, Reinhard C, Randazzo F, Crkenjakov R, Drmanac S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 910; 1046pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-1999;
02-JUL-1999;
                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human polynucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF66728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF66728 standard; cDNA; 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000; 2000WO-US18374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast cancer; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 TTATCTTCAATTTAT 188
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ggtattgtaaatgtg
                                                                          l Similarity
15; Conserv
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                                                                                                                                                                                                  377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garcia V,
                                                                                                                                                                                                                                                and
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                             hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0142310.
99US-0142311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; colon cancer; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; cancer detection; ss.
                                                                                              12.2%;
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Dickson M, Labat I
S LW, Strache-Crain E
                                                                                                                                                                                               ე
                                                                          0;
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                                                                                              Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
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                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                               <u>ი</u>
                                                                                                                                                                                               128
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Pot D, L
Labat I,
ne-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2484.
                                                                                              DB
91;
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, Lamson G, Drmanac
                                                                                                                                                                                                  other
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                                                                                                                     Length 377;
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                                                                          Indels
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nanac R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or a
                                                                       Gaps
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RESULT 41
AAF66301/c
ID AAF663
XX AAF663
XX AAF663
XX Novel
XX Novel
XX Human;
KW breast
XX Homo s
PN W02001
XX 11-JAN
XX 02-JUI
PR 02-J
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                                                                                                                                                                                                                                                                                                                       The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and produce antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia,
                                                                                                            Matches
                                                                                                                                      Best Local
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams LT, ESCUDENT Reinhard C, Randazzo F, F Reinhard C, Randazzo F, F Crkenjakov R, Drmanac S, Crkenjakov R, Jones
                                                                                                                                                                                                                                            Sequence 391 BP; 85 A; 105 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 842; 1046pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon
                                                                                                                                                                                                                                                                                                   dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-091805/10
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02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
(CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                            l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprises 3351 human polynucleotide sequences
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide,
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99US-0142311
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                                                      70
  91
                                                                                                                                100.0%;
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Kennedy GC,
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Kennedy GC, Pot D, Lamson
Dickson M, Labat I, Leshk
LW, Strache-Crain B;
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                                                                                                                                      Score 15;
Pred. No.
                                                                                                                                                                                                                                               130 G;
                                                                                                               Mismatches
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                                                                                                                                                                                                                                                  Η.
                                                                                                                                      91;
                                                                                                                                                            DB 22; Length 391;
                                                                                                                                                                                                                                                  0 other;
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mson G, Drmanac R;
Leshkowitiz D;
                                                                                                            Indels
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RESULT 42 AAF66405/c

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RESULT
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Best Local
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Reinhard C, R
Crkenjakov R,
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 06-OCT-2000
                                             762
                                                                                                                                                                      antibodies against them can be used in pharmaceutical compositic treat the cancers and proliferative disorders such as neoplasia dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                           Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                   AAC01762;
                                   AAC01762 standard;
                                                                                                                                                               Sequence 412
                                                                                                                                                                                                                  blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and
                                                                                                                                                                                                                                                                                                                            Claim
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02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human polynucleotide,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                                         gctgcactgactggt 74
                                                                                GCTGCACTGACTGGT 319
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                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                   l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic;
cancer; lung
                                                                                                                                                                                                                                                                                                                                                                                                s LT, Escobedo J,
d C, Randazzo F,
kov R, Drmanac S,
Garcia V, Jones
                                                                                                                                                                                                                                                                                                                           Page 859; 1046pp; English.
                                                                                                                   Conservative
                                                                                                                                                               BP;
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0142310
                                                                                                                                                              113 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; colon cancer;
g cancer; cancer detection; ;
                                    CDNA; 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cdna;
                                                                                                                           12.2%;
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Dickson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412
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                                                                                                                  0;
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                                                                                                                           Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                              85 G;
                                                                                                                                                                                                                                                                                                                                                                                               nis MA, Garcia PD,
nedy GC, Pot D, L
ckson M, Labat I,
Strache-Crain B;
                                                                                                                   Mismatches
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                                                                                                                           91;
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                                                                                                                                   22;
                                                                                                                                                               0
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                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss.
                                                                                                                                   Length 412;
                                                                                                                  Indels
                                                                                                                                                                                                  compositions
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                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 Kassam
anac R;
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                                                                                                                 Gaps
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OSXXXX DEXXX
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                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                   Query Match
Best Local :
Fusarium venenatum
                 metabolic
                                                                                                                                                                                                                                                                                                                                                                                        The
                                                                                       13-MAR-2001
                                                                                                        AAF10271;
                                                                                                                                                                                                                                                                                                                                                                      sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEST
                                                                                                                                                                       375
                                                                                                                                            44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted
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derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recomb culture condition; environmental stress; spore morphogenesis;
                                                                                                                                       Fusarium venenatum EST SEQ ID NO: 2794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID 1760; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                           AAF10271 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic, forensic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     87 taaggtgatacttat 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence
As encoding secret
                                                                                                                                                                                                                                                                                                                                                                                           TAAGGTGATACTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5' EST;
condition; ic pathway e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 123 A; 116 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equence is one of a large number of 5' ESTs derived from secreted proteins. An ORF has been identified within the 5' ESTs were prepared from total human RNAs or polyA+ RNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome
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  engineering;
                                                                                                                                                                                                                                                                           cDNA;
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                           556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tag;
mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15;
Pred. No.
                                                                                                                                                                                                                                                                           ВP
    catabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
91;
spore morphogenesis;
pathway engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T; 1 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         umber of 5' ESTs derived from has been identified within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tag (5' EST) for to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                              recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RRESULT 4
AAC87968
ID AAC87978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for monitoring differential CC expression of genes in a first filamentous fungal (FF) cell relative to cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the CC same genes in one or more second filamentous fungal cells. Monitoring CC the global expression of genes from FF cells allows the production CC potential of the microorganisms to be improved. New genes may be CC identified and gene copy number variation and stability can be comproduced, possible functions of unknown open reading frames can be cC identified and gene copy number variation and stability can be cC adapt to changes in culture conditions, environmental stress, spore CC monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore CC morphogenesis, recombination, metabolic or catabolic pathway CC engineering. Using ESTs provides several advantages over genomic or array equals one gene or open reading frame, and organisation of the CC microarrays based on function of the gene products to facilitate CC analysis of the results. AAF07478 to AAF11247 represents ESTs from Aspergillus or catabolic catabolic pathway. AAF11248 to AAF11247 represents ESTs from Aspergillus or catabolic catabolic pathway. AAF14879 to AAF14879 to AAF14879 to AAF1337 represents ESTs from Trichoderma reesei, which are CC all specifically claimed in the present invention.
CLASP-1; CLASP-2; transmembrane protein; immune response; inflammatory; cadherin-like asymmetry protein; autoimmune disease; immunosuppressive; immunomodulatory; antiinflammatory; antiarthritic; cytostatic; hypotensive; antirheumatic; antianaemic; haemostatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human CLASP-2
                                                                                                                                                                                                                              07-MAR-2001
                                                                                                                                                                                                                                                                                            AAC87998;
                                                                                                                                                                                                                                                                                                                                                       AAC87998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 556 BP; 160 A; 128 C; 138 G; 128 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 86; Page 1396; 3161pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 aatggcgcaatgcga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                       standard; DNA; 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                genomic DNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9905-0273623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.2%;
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                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15;
Pred. No.
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                                                                                                                                                                BAC ref 13.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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used to inhibit an immune response in a subject by interfering with th ability of a CLASP-2 protein to bind to another T cell or B cell. An immune response in a subject may also be inhibited by administering an antibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, proteins and antibodies can be used to prevent or treat a CLASP-2 mediated disease, such as an autoimmune disease caused or exacerbated by increased activity of THII cells. They can also be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1999;
14-MAY-1999;
21-OCT-1999;
                                                                                                      hypersensitivities, prevent transplantation rejection responses and augment immune responsiveness in immunodeficiency states, inhibit proliferation and differentiation of cells involved in an inflammatory response e.g. arthritis, inflammatory bowel disease and increase differentiation and proliferation of haematopoietic cells e.g. to treat anaemia, thrombocytopaenia and other blood protein disorders. Disorders treated by disrupting CLASP-2 function include multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypersensitivity; transplantation rejection response; immunodeficiency; proliferation; differentiation; inflammatory response; arthritis; inflammatory bowel disease; haematopoietic cell; blood protein disorder; anaemia; thrombocytopaenia; multiple sclerosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                           antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antianaemic, haemostatic and neuroprotective activities. CLASP-2 can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
Sequence
                                                    rheumatoid arthritis, endometriosis and pregnancy induced hypertension. The present sequence represents a human CLASP-2 genomic DNA sequence from a bacterial artificial chromosome (BAC), given in the present
                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes cadherin-like asymmetry protein-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated cadherin-like asymmetry protein-2 polynucleotide and polypeptide used to diagnose, treat and prevent autoimmune di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lu PS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endometriosis; pregnancy induced hypertension; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example
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14-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                             (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ARBO-)
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     567
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 6A; 286pp; English
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99US-0134117
99US-0134118
99US-0160860
99US-0162498
99US-0170453
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2000US-0176195
 ВP;
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   161 A; 89
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     188
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     24 other;
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98 70

Query Match Best Local Matches

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Similarity

100.0%;

Score 15; Pred. No

90 80

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Length 567;

Page 24

Job time: 2912 sec

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Minimum
Maximum
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-09-157-177-111
US-09-157-17-23
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Compugen Ltd.
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Sequence 27, Appl
Sequence 27, Appli
Sequence 2, Appli
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Sequence 213, App
Sequence 297, Appli
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Sequence 2, Appli
Sequence 70, Appli
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10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	11.4
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Sequence 12, Appl	Sequence 12, Appl	Sequence 21, Appl			Sequence 50, Appl			Sequence 133, App	Sequence 133, App	Sequence 3, Appli	Sequence 316, App	Sequence 315, App	Sequence 316, App	Sequence 315, App	Sequence 14, Appl	Sequence 16, Appl	Sequence 101, App

## ALIGNMENTS

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APPLICANT: No. 6197505berg, Leif T
APPLICANT: Andersson, Maria K
APPLICANT: Linstrom, Per H
APPLICANT: Linstrom, Per H
TITLE OF INVENTION: Per ASSESSING CARDIOVASCULAR STATUS AND
TITLE OF INVENTION: COMPOSITIONS FOR USE THEREOF
FILE REFERENCE: 1248/1D042
CURRENT APPLICATION NUMBER: US/09/050,159A
CURRENT FILING DATE: 1998-03-27
EARLIER FILING DATE: 1987-04-03
NUMBER OF SEQ ID NOS: 133
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1278
TYPE: DNA
OPENION: USE OF SEC ID NOS: 137
SEQ ID NO 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Anglotensinogen, US-09-050-159-123
                                                                                                                                                                           Sequence 12, Application US/09069886 Patent No. 6132724 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 123, Application US/09050159A Patent No. 6197505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
                                                              APPLICANT: Blum, Kenneth
APPLICANT: Comings, David E.
APPLICANT: Ivy, John L.
TITLE OF INVENTION: ALLELIC POLYGENE DIAGNOSIS OF REWARD
TITLE OF INVENTION: DEFICIENCY SYNDROME AND TREATMENT
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                         522 TGGTAAGTTTCACATG
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Pred. No.
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US-09-069-886-27; Sequence 27, Application US/09069886; Patent No. 6132724
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Best Local Similarity
Matches 15; Conser
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hodgins, Daniel S.
REGISTRATION NUMBER: 31,026
                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/069,886
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                               REFERENCE/DOCKET NUMBER: BL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (512)418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: IVY, John L.
TITLE OF INVENTION: ALLELIC POLYGENE DIAGNOSIS OF REWARD
TITLE OF INVENTION: DEFICIENCY SYNDROME AND TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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                                TELEPHONE:
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ZIP: 77210-4433
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STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
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(512)474-7577
DR SEQ ID NO:
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                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                               TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
307 TAAGGTGATACTTAT 293
                        87
                                                                                                                         CLONE:
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TYPE: nucleic acid .
STRANDEDNESS: single
                                                                                                                         CLONE: 1649584
                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc STREET: 3174 Porter Drive
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                                                             Score 15;
Pred. No.
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Pred. No.
                                                 Mismatches
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US-09-212-167-2
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                                                                                                                                                            Sequence 1, Application PC/TUS9509261 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1099 base pairs
TYPE: nucleic acid
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 TITLE OF INVENTION:
                              APPLICANT:
                                                                         APPLICANT:
                                                                                                     APPLICANT:
                                                                                                                    APPLICANT:
                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 415-855-0555
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                    307 TAAGGTGATACTTAT 293
                                                                                                                                                                                                                                                                     87 taaggtgatacttat 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/212,167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415-845-4166
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                                                          COUNTRY: Un:
POSTAL CODE:
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                              TELEFAX:
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                                                                                                                                  NAME:
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                             TELEPHONE NO: (512)499-4462
TELEFAX: (512)499-4523
                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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METHODS AND COMPOSITIONS FOR THE EXPRESSION OF A BONE AND PROSTATE DERIVED GROWTH FACTOR
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                                                          United States of America
DE: 78701
                                                                                                   201 West 7th Street
Austin
                                                                                                                               BOARD OF REGENTS, THE UNIVERSITY OF TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08/871,033
                                                                                       Texas
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; LOCATION:
PCT-US95-09261-1
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                                SEQ ID NO 111
LENGTH: 528
                                                                                                                                                                                                                                                                                            GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                            Sequence 111, Application US/09157177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                   APPLICANT: MONFORTE, JOSEPH A.
APPLICANT: Becker, Christopher H.
TITLE OF INVENTION: DAN TYPING BY MASS SPECTROMETRY WITH
TITLE OF INVENTION: REPEAT MARKERS
FILE REFERENCE: GETR: 017/GETR017/P
CURRENT APPLICATION NUMBER: 05/09/157,177
CURRENT FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                         Patent No. 6090558
                                                                                                EARLIER APPLICATION NUMBER: 60/059,415
EARLIER FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                         APPLICANT: Butler, John M. APPLICANT: Li, Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
                                                                 SOFTWARE: PatentIn Ver.
                                                                                 NUMBER OF SEQ ID NOS: 135
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  3143 AATTTATTCCACACA 3129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: SERTICH, GARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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TOPOLOGY: linear
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                                 528
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694..2310
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SYSTEM: PC-DOS/MS-DOS/ASCII
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US-09-328-111-297
; Sequence 297, Application US/09328111
; Patent No. 6262333
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APPLICANT: Lewis, Marcia E.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

CURRENT APPLICATION NUMBER: US/09/328,111

CURRENT FILING DATE: 1999-06-08

FEARLIER APPLICATION NUMBER: US 60/088,801

EARLIER FILING DATE: 1998-06-10

NUMBER OF SEQ ID NOS: 850

SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(564)

; OTHER INFORMATION: n = A,T,C or G

US-09-328-111-223
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LENGTH: 564
TYPE: DNA
                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT:
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mes 14; Conserv
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0. 6262333
                                            Endege, Wilson O.
Steinmann, Kathleen E.
Astle, Jon H.
Burgess, Christopher C.
Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
Derti, Adnan
Ford, Donna M.
Lewis, Marcia E.
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                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No.
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Pred. No.
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67;
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67;
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              IMMEDIATE SOURCE:
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; NAME/KEY: misc_feature
; LCCATION: (1)...(574)
; OTHER INFORMATION: n = A,T,C
US-09-328-111-297
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EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 297
LENGTH: 574
TYPE: DNA
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Best Local Similarity
                                                                                APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECHOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL HUMAN GENES TITLE OF INVENTION: PRODUCTS FILE REFERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Monahan, John E. APPLICANT: Schlegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, J
TITLE OF INVENTION: N
TITLE OF INVENTION: S
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/8 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
STRANDEDNESS:
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                                   LENGTH:
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          : 750 base pairs nucleic acid
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NEW HUMAN NADH DEHYDROGENASE
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Pred. No.
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TOPOLOGY:

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RESULT 12
US-08-989-289-2
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 Sequence 2, Application US/08989289 Patent No. 5968747 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 14; Conservative
                                                                                                                                                        Matches
                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hillman, i
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                                                                  641 TTGTAAATGTGAGA 654
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                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/208,210 FILING DATE: .
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ilarity 100.0%;
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NEW HUMAN NADH DEHYDROGENASE
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Pred. No.
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67;
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Best Local Similarity 100.
                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Benton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                        APPLICANT: Lee, Ving
APPLICANT: Malouin, Frai
APPLICANT: Martin, Patr:
APPLICANT: Schmid, Moll)
APPLICANT: Sun, Dongxu
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LENGTH: 877 base pairs
TYPE: nucleic acid
                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION UNBER: US/08/989,289 FILING DATE: Herewith
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APPLICANT: Corley, Neil C.
TITLE OF INVENTION: UBIQUI
NUMBER OF SEQUENCES: 3
                                                                   CORRESPONDENCE ADDRESS:
                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,7
REFERENCE/DOCKET NUMBER:
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OPERATING SYSTEM:
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Los Angeles
California
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                       Suite 4700
                                       E: Lyon & Lyon
633 West Fifth Street
                                                                                                                                     Lee, Ving
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
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                                                                                                            STAPHYLOCOCCUS AUREUS
                                                                                                                                                                                                                                                                                                                                                                                11.4%; Score 14; 100.0%; Pred. No.
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67;
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2;

Length 877; Indels

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Gaps

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ANTIBACTERIAL

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskett
MEDIUM TYPE: storage
COMPUTER: IBM Compatible

Diskette, 1.44 Mb

COUNTRY:

RY: U.S.A. 90071-2066

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TELEFAX: (213) 955-0440
TELEEX: 67-3510
INFORMATION FOR SEQ ID NO: 70
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 70, Patent No. 6
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Best Local 9
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                                                                                                                                                                                                                                 APPLICANT: Sun, Dongs
TITLE OF INVENTION: N
TITLE OF INVENTION: T
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA
                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA
APPLICATION UMBER: 60/009,102
FILLING DATE: December 22, 1995
APPLICATION NUMBER: 60/03,798
APPLICATION NUMBER: 60/03,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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                                                                                                                                                                    STREET: 633 West F
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: SIT
                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                       CITY: Los Angeles
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REFERENCE/DOCKET NUMBER: 222/005
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14; Conservative
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Malouin, Francois
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Pred. No.
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 70
                   SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/26
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/714,9
FILING DATE: September 13, 1
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: Septembe
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                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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FILING DATE: Decembe
APPLICATION NUMBER:
FILING DATE: Septemb
                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: sing
                                                                                                                                                     OPERATING SYSTEM: IBM P.C.
                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 90071-2066
        APPLICATION NUMBER:
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Malouin, Francois
Martin, Patrick K.
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60/009,102
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per 22, 1995
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                                       08/714,918
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ber 13, 1996
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Pred. No.
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RESULT 16
US-09-266-417-70/c
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                                        FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/;
FILING DATE: March 9, 1999
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TITLE OF INVENTION:
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REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
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523 GGTATTGTAAATGT 510
                                                                         FILING DATE: September:
APPLICATION NUMBER:
FILING DATE: December
APPLICATION NUMBER:
                                                                                                                                                                                                                                OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                        STREET: 633 West
STREET: Suite 470
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213) 489-16
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 90071-2066
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                           NAME: Warburg, Richard J.
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 REFERENCE/DOCKET NUMBER:
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5. 6228588
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pedness: single
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                                                                                                                                                                                                                                                                                                                                                           California
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633 West Fifth Street
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                               IBM Compatible
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                                                                                          December
                                                                                                         September 13, 1996
UMBER: 60/009,102
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JMBER: 60/003,798
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                                                                          er 22, 1995
60/003,798
                                                                                                                                      08/714,918
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240/248
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Pred. No.
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68;
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US-08-874-186-37/c
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GENERAL I
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Best Local
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SEQUENCE CHARACTERISTICS:
LENGTH: 1021 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 0
PRICING DATE: 10-JAN-1997
                                                                                                                                                                                                                            FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Teng, David H-F.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Perry III, William L.
APPLICANT: Skolnick, Mark H.
                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4848
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                              FEATURE:
                                                         MOLECULE TYPE: HYPOTHETICAL:
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                                            ANTI-SENSE:
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523 GGTATTGTAAATGT 510
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TELEFAX: (213) 955-0440
TELEX: 67-3510
              NAME/KEY:
                                                                                                      STRANDEDNESS:
                                                                                                                                    LENGTH:
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5989885
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                                                                                                                    nucleic acid
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                                                                                                                                    1620 base pairs
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                                              NO
                                                                                         linear
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                                                              NO
                                                                          DNA (genomic)
                                                                                                         double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIFIC MUTATIONS OF MAP KINASE KINASE 4 (MKK4) IN HUMAN TUMOR CELL LINES IDENTIFY SUPPRESSOR IN VARIOUS TYPES OF CANCER
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Pred. No.
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Best Local Similarity
Matches 14; Conserv
                                                        Matches
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                                                                                 Query Match
                                                                                                                                                                                                                                                                       TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: OSMAD, Richard Aron,
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59767/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Destruelle, Monika
APPLICANT: Holzer, Helmut
TITLE OF INVENTION: NUTRIENT I
                                                                                                                                                                                     MOLECULE TYPE:
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NAME/KEY:
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||||||||||||||
269 TGTAAATGTGAGAT 256
                                                                                                                                          NAME/KEY:
LOCATION:
           14 tgtgagatgcctta 27
                                                     Local Similarity 100 nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/222,289 FILING DATE: 04-APR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                             STRANDEDNESS:
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TGTGAGATGCCTTA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                            nucleic acid
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                                                                                                                                                                                                                                         2165 base pairs
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370..1434
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1326..1428
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100.0%;
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100.0%;
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Pred. No.
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Pred. No.
                                                       Mismatches
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                                                                    DB 1;
69;
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68;
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                                                                                 Length 2165;
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RESULT 20
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5194375-5
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                                                                                                                                                                                                       ;Patent No. 5194375
APPLICANT: PARK, LINDA S.;GOODWIN, RAYMOND G.
TITLE OF INVENTION: DNA ENCODING INTERLEUKIN-7 RECEPTORS AND
METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                               SEQ ID NO:5
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Patent No. 5648240
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APPLICANT: 1
APPLICANT: 1
APPLICANT: 1
APPLICANT: 1
APPLICANT: 1
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                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   2169 TGTGAGATGCCTTA 2156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/248,021A FILING DATE: 24-MAY-1995 CLASSIFICATION: 424 CLASSIFICATION: 424
                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: TA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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NAME: Kitchell, Barbara S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                               APPLICATION NUMBER: 421,201 FILING DATE: 13-OCT-1989 APPLICATION NUMBER: 366,910
                                                                                                                                                                                                                                                                                                                                                                  14 tgtgagatgcctta 27
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
              LENGTH: 2466
                                               FILING DATE: 15-JUN-1989
                                                                                                                                   APPLICATION NUMBER: US/
FILING DATE: 21-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Houston
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Jonsson, Klas
Patti, Joseph M.
Patti, Joseph M.
Patri, Joseph M.
Patring FROM S
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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100.0%; Pr
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Pred. No.
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RESULT 22
US-09-079-587-2/c
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                                                          Sequence 2, Application US/09079587 Patent No. 6130066
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Patent No. 5990091
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                            GENERAL INFORMATION: APPLICANT: TARTAG
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                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-588-0500 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 APPLICANT:
                                                                                                                                              1759 ATTTATTCCACACA 1746
                                                                                                                                                                                                                                                                                          TOPOLOGY: li
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REFERENCE/DOCKET NUMBER: 454310-2990
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION,
TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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STATE: NEW YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: KOWALSKI, THOMAS J. REGISTRATION NUMBER: 32,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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FILING DATE: 12-MAR-1997
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                                                                                                                                                                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                                                                                                                                                                 4259 base pairs
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COX, WILLIAM I.
GETTIG, RUSSELL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                              212-588-0500
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                              TARTAGLIA, JAMES
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69;
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US-08-685-871-1
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Best Local S
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                                                                                                COUNTRY:
                                                                                                                                            STREET:
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Sequence 1, Application US/08685871 Patent No. 6013499 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
APPLICATION NUMBER: 12-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
          COMPUTER READABLE FORM:
MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                 1759 ATTTATTCCACACA 1746
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TELECOMMUNICATION INFORMATION: 212-588-0800
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MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 atttattccacaca 120
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                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                   E: Foley & Lardner
3000 K Street, N.W., Suite 500
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llarity 100.0%;
Conservative
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                Version
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RESULT 24
US-08-342-930-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4739 harr
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Best Local Similarity
APPLICATION NUMBER: US/08/342,930
FILING DATE: 21-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-20975.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                        CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 7-262553 FILING DATE: 14-SEP-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIOR APPLICATION DATA:
                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                 94304-1018
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448..4509
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24-JUL-1996
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Pred. No.
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-112-450-3
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Best Local S
Matches 14
                                                                                                                                                                                            Sequence 1, Application US/08816155B Patent No. 5990091
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/112,450 CURRENT FILING DATE: 1998-07-09 EARLIER PLICATION NUMBER: 60/052,273 EARLIER FILING DATE: 1997-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Abad, Antonio Jose C.
APPLICANT: Chol, Gil
APPLICANT: Calderone, Richard A.
TITLE OF INVENTION: Histidine Kinase Two-component in Candida albicans
FILE REFERENCE: PF393
                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 60/0EARLIER FILING DATE: 1998-02-11
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 8561
                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                       1667 AGGTATTGTAAATG 1654
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                          CORRESPONDENCE ADDRESS:
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            ADDRESSEE:
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                                        MARTINEZ, HECTOR
PAOLETTI, ENZO
PINCUS, STEVEN E.
VECTORS F
NVENTION: METHODS (
SEQUENCES: 48
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                                                                                                                                    GETTIG, RUSSELL R.
                                                                                                                                                  COX, WILLIAM I
                                                                                                                                                                                                                                                                                                                                                  Conservative
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FROMMER LAWRENCE & HAUG LLE
5 FIFTH AVENUE
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100.0%; Pr
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; Pred. No.
                                                        HAVING ENHANCED EXPRESSION, OF MAKING AND USES THEREOF
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                  Mismatches
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70;
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COMPUTER READABLE FORM:

10151

COUNTRY:

NEW YORK

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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 10281 base pairs
TYPE: nucleic acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIEN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,155E
EILING DATE: 12-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REFERENCE/DOCKET NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-29
TELLCOMMUNICATION INFORMATION:
TELEPHONE: 212-888-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                              COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MARTINEZ, HECTOR
APPLICANT: PINCUS, STEVEN E.
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION,
TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1788 ATTTATTCCACACA 1775
            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/816,155
FILING DATE: 12-MAR-1997
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 FIFTH AVENUE
                                                                                                                     CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                               CITY: NEW YORK
                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                              STATE:
                                                                  CLASSIFICATION:
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GETTIG, RUSSELL R.
                                                                                                                                                                                                                                            USA
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71;
                                                                                                                                     #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 101,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                 TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                            SOFTWARE: PACELLE SOFTWARE: PACELLE DATA:
CURRENT APPLICATION NUMBER: US/08/742,185
APPLICATION NUMBER: 30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1788 ATTTATTCCACACA 1775
                                                                                                                                REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                               FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 01 FILING DATE: 31-JUL-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 01
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEPHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DAZ: A NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 NAME: Granahan, Patricia REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 10281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08742185 6020476
                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Hamilton, Brook, Smith & Reynolds, P.C
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212-588-0500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reeve, Mary Pat
                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hawkins, Trevor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saxena, Richa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reijo, Renee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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DNA (genomic)
                               single
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100.0%; PJ
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                                                                                                   101:
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US-08-427-569-14/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Patton, David A.
APPLICANT: Ashby, Carl S.
APPLICANT: Thomas, Carla R.
APPLICANT: McElver, John A.
APPLICANT: Budziszewski, Gregory J.
APPLICANT: Levin, Joshua Z.
APPLICANT: Levin, Joshua Z.
TITLE OF INVENTION: Herbicide Target Genes and Meter File Referrence: PB/5-30825.
CURRENT APPLICATION UMBER: US/09/503,391
CURRENT FILING DATE: 2000-02-14
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                                                                                                                                                         Patent No. 6235465
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08427569 Patent No. 6235465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/09503391 Patent No. 6300091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
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SEQ ID NO 16
LENGTH: 30
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                 APPLICANT: Kolberg, Janice A.
APPLICANT: Urdea, Michael S.
TITLE OF INVENTION: HTLV-1 PROBES FOR USE IN SOLUTION
TITLE OF INVENTION: PHASE SANDWICH HYBRIDIZATION ASSAYS
NUMBER OF SEQUENCES: 55
                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             COUNTRY:
                                                                                                                                                                                CITY: Palo Alto
                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Conservative
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                                                                                                                            94304-1018
                                                                                                                                                              California
                                                                                                                                                                                           E: Morrison & Foerster
755 Page Mill Road
                                                                                                                                               USA
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100.0%; Pred. No.
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100.0%;
US/08/427,569
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Pred. No.
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72;
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                                   #1.25
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RESULT 31
US-08-311-760A-315
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Best Local Similarity 100.0%;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                   OPERATING SYSTEM: IBM P.C. I
SOFTWARE: FastSEQ Version 1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   STREET: 633 West STREET: Suite 4700 CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                             APPLICATION NUMBER: US/08/311,71
FILING DATE: September 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ramharack, Randy
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Ciotti
                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 gatgccttacaac 31
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/C
FILING DATE:
APPLICATION NUMBER: 07/8
FILING DATE: 23-DEC-1931
                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 90071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15, Application US/08311760A
5599706
                                                                                                                                                                                                                                                                                                                                                                                                                         633 West Fifth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stinchcomb, Dan '
McSwiggen, James
Newton, Roger S.
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                                                                                                                                                                                                                                                       IBM Compatible
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                                                                                                                                                                                                                                          DOS 5.0
                                                                                                                                                                                                                                                                                               1.44 Mb
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-311-760A-315
                                                 US-08-311-760A-316
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US-08-311-760A-316
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/311,760A

FILING DATE: September 23, 1994

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                              TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stinchcomb, Dan T. APPLICANT: McSwiggen, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 633 web. ..
STREET: Suite 4700
STREET: Annaeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Los Angeles
: California
                                                                                             nucleic acid
                                                                                                              36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Lyon & Lyon
633 West Fifth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ramharack,
                                                               linear
                                                                                single
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84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIBOZYME TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF PLASMA LIPOPROFEIN (a) [LP(a)] BY INHIBITING APOLIPOPROTEIN
10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13; DB 1;
Pred. No. 2.3e+02;
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Score 13;

DB 1;

Length 36;

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RESULT 34
US-08-774-310-316
; Sequence 316, Application US/08774310
; Patent No. 5877022
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US-08-774-310-315
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Matches 11; Conserva
                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                              TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Ramharach
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/774, FILING DATE: December 23, 1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/311,760 FILING DATE: September 23, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                            27 acaaccctgatga 39
                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Version 1.5
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STATE: California
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                                                                                             2 ACAACCCUGAUGA 14
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                                                                                                                                                                                                                                                                               36 base pairs
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633 West Fifth Street
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McSwiggen, James
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                                                                                                                                                   Score 13; DB
Pred. No. 2.3e
2; Mismatches
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2; Mismatches 0;
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2.3e+02;
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                                                                                                                                                                                Length 36;
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INFORMATION:

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US-08-207-226A-3/c
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                                                                                                                                                                                                Sequence 3, Application US/08207226A Patent No. 5580970
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Best Local Similarity
                                                                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                             APPLICANT: Hendricks, David
APPLICANT: Rigby, Susan
APPLICANT: Parodos, Kyriaki
TITLE OF INVENTION: DETECTION OF
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatition
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
1006
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LENGTH: 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/774,31
FILING DATE: December 23, 1996
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/311,760
FILING DATE: September 23, 1994
ATTORNEY/AGENT INFORMATION:
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                  CITY: Naperville
                                 STREET:
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                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
Illinois
                                 E: Amoco Corporation
55 Shuman Boulevard, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                      10.6%; Score 13;
84.6%; Pred. No.
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                                                                                                           HPV TRANSCRIPTS
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US-08-425-684-133/c
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US-08-425-684-133
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APPLICATION NUMBER: 07/622,742
FILING DATE: 05-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5580970val B
REFERENCE/DOCKET NUMBER: GTR-890:
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 133, Application US/08425684 Patent No. 5834252
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Best Local (
                                                                                                       TELEFAX: (415) 326-24 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                        NAME: DUNN ESQ., TRACY J.
REGISTRATION NUMBER: 34.587
REFERENCE/DOCKET NUMBER: 16:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
STREET: ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: STEMMER PH.D., WILLEM P.C.
TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                  STRANDEDNESS:
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/425,684 FILING DATE: 18-APR-1995 CLASSIFICATION: 435
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CLASSIFICATION:
                                                                     LENGTH:
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13; Conserv
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                                                                    40 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                  circular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                          326-2422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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RESULT 38
US-09-129-740-10/c
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Sequence 10, Application US/09129740A Patent No. 6067246
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MURPHY, ESQ., MATTHEW B. REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 16528J-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 336-2420
TELEPAX: (415) 336-2422
INFORMATION FOR SEQ ID NO: 133:
                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 133, Application US/08675502 Patent No. 5928905
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/425,684
FILING DATE: 18-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/US96/05480
FILING DATE: 18-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: STEMMER PH.D., WILLEM P.C.
APPLICANT: LIPSHUTZ, ROBERT J.
TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                     111 attccacacaaca 123
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                                                                                                                 21 ATTCCACACAACA 9
                                                                                                                                                                                         Local Similarity les 13; Conserv
                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/675,502 FILING DATE: 03-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                           circular
                                                                                                                                                                                                           10.6%; Score 13; DB 2; L
100.0%; Pred. No. 2.3e+02;
                                                                                                                                                                                         0;
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Pred. No. 2.3e+02
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US-08-821-559A-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1997-08-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17,
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Best Local Similarity
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                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Kettelberger, Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 8648.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DNA OPTICAL STORAGE FILE REFERENCE: DAVID B. MURPHY - Heller 236/119 CURRENT APPLICATION NUMBER: US/09/129,740A CURRENT FILING DATE: 1998-08-05 EARLIER APPLICATION NUMBER: 08/906,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HELLER, MIC APPLICANT: TU, EUGENE
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: XIA, YU. TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3100 No. 9
CITY: Minneapolis
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                                TOPOLOGY:
                                                STRANDEDNESS:
                                                                                                                                                  TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 21-MA
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                                                                 nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Merchant, Gould, Smith, Edell, Welter & Schmidt 3100 No. 5846774west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                                                       21-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette
                                            single
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v 100.0%; Pr
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PCT-US95-14418-50
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
COMPUTER READABLE FORM:
                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 15
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                          111 attccacacaaca 123
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                                                              STREET:
                                                                                                                                                                                                                                                                        57 ATTCCACACAACA 69
                  COUNTRY:
                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                 Chicago
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pedness: single
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           Illinois ... United States of America
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                                                           E: Marshall, O'Too
6300 Sears Tower,
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6300 Sears Tower,
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                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                        Biologically Active Fragments of
Thermus Flavus DNA Polymerase
                                                                                                                                                                                                                                                                                                                                                   10.6%;
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                                                             O'Toole, o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O'Toole, Gerstein, Murray & Borun ower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50:
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Pred. No.
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; Mismatches
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                                                             Gerstein, Murray & Borun
South Wacker Drive
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hes 0;
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                                                                                                                                                                                                                                                                                                                                    Indels
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                             INFORMATION FOR SEQ ID NO:
                                           SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUMANISED ANTIBODIES NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: GASS, DAVID A.
REGISTRATION NUMBER: 38,:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             STREET: One L. CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 attccacacaaca 123
                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                        TELEPHONE:
                                                                                                                                                        NAME: Trujillo, Doreen REGISTRATION NUMBER: 3
                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/
FILING DATE: 25-March-1996
                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                               TYPE:
                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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COMPUTER: II
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                             nucleic acid
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                                                                                          (215)
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              single
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35,719
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ER: 28003/31716
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Pred. No.
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2.3e+02
           Length 70;
Indels
0
Gaps
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0

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: No. 6180377ris, LLP Version #1.25 (EPO)

FILING DATE:

03-JUN-1994

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LENGTH: 95
; TYPE: DNA
; ORGANISM: Deinococcus radiophilus
US-09-235-246-21
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US-09-235-246-21/c
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CURRENT APPLICATION NUMBER: US/09/235,246A
CURRENT FILING DATE: 1999-01-22
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12,
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Matches 13; Conserv
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Best Local Similarity 100.0%;
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APPLICANT: Higgins, Lauren S.
APPLICANT: Ditton, Michael A.
APPLICO, INVENTION: Method For Cloning And Producing The DraIII Restriction
TITLE OF INVENTION: Endonuclease
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        tent No.
             ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: American
                                                                                                                                                                                                                         TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor TITLE OF INVENTION: Agents and Intermediates for Their Synthesis NUMBER OF SEQUENCES: 73
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                                                                                                                                 STATE: Wayne
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APPLICATION NUMBER:
                                                                                                                              STATE: New Jersey COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 ATTCCACACAACA 45
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                                                                                                                                                                           One Cyanamid Plaza
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Holcomb, Ryan
Hallett, William
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US/08/253,877C
                                                                                                                                                                                           Cyanamid Company
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RESULT 45
US-08-452-164A-12/c
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SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12,
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Best Local Similarity
                                                                           TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 530
                                                                                                                              TELEPHONE: 201-683-2158
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                    STREET: UNC
STREET: UNC
CITY: Parsippany
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Conjugates of Melhyrtrand ......TITLE OF INVENTION: Agents and Intermediates for Their Synthesis with the of SEQUENCES: 73
                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
 TOPOLOGY: 1
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                           REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
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REFERENCE/DOCKET NUMBER: 32,368
                            TYPE: nucleic acid
STRANDEDNESS: single
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                                                               96 base pairs
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Weiss, Martin J.
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Hallett, William
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                linear
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DNA (genomic)
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Pred. No.
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hes 0;
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Query Match
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 agatgccttacaa 30
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Db 78 AGATGCCTTACAA 66

Search completed: March 19, 2002, 11:04:27

Job time: 3856 sec
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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gb_htg:*
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em_htgo_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No	Score	+ 10 B	ngt 903	8 B	ID ATT22F8	cription 50351 Ara
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		23.4	07 53	ο ω ω μ	00115 00271 00473	52 17 35

## ALIGNMENTS

TITLE	REFERENCE	JOURNAL		AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	ATT22F8/c	RESULT 1
EU Arabidopsis sequencing, project. Direct Submission	2 (bases 1 to 89035)	Unpublished	Mewes, H.W., Mayer, K.F.X. and Schueller, C.	Bevan, M., Zimmermann, W., Grueneisen, A., Wambutt, R., Bancroft, I.,	1 (bases 1 to 89035)	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Arabidopsis thaliana	thale cress.		AL050351.1 GI:4914422	AL050351	project).	Arabidopsis thaliana DNA chromosome 4, BAC clone T22F8 (ESSA	ATT22F8 89035 bp DNA PLN 27-MAY-1999		

/gene="T22F8.20" /gene="T22F8.20" /note="similarity to Mono-phosphatase, Streptomyces anulatus, x92429 Contains Inositol monophosphatase family signatures [WVLDFIDGTKSFIT][VLDFIDGTKSFIT]" /codon_start=1 /product="Inositol monophosphatase-like protein" /protein_id="CAB43627.1" /db_xref="git.4914424" /translation="MASNSKRPNISNESPSELSDTELDRFAAVGNALADASGEVIRKY FRKKFDIVDKDDMSPVTIADOMAEEAMVSIIFQNLPSHAIYGEEKGWRCKEESADYW VLDPIDGTKSFITGKPVFGTLIALLYKGKPILGLIDQPILKERWIGMNGRRTKLNGED	/gene="T22F8.20" /number=1 /number=1 complement(join(82 9059. 9125,9296. 1024210413) /gene="T22F8.20" complement(join(82 90599125,9296. 1024210413))	LQLQEAFTQGKAEETENAKPDVVTPGSVPVSDPSPITPSVTTNEAATVPVPAKVEENS GTAVDEHSGTAMFTQFANLNGR"  exon	/db_xref==G1:4914423*  /db_xref==G1:4914423*  /taanslatlon="Meirkkenifftvluidesskermalllailletsgersavana / traanslatlateresgersavana / traanslatlon="Meirkkenifftyluidesskermalllailletsgersavana avgertagekermaldetildcgsksssktpdgrteksdetiqyteakediqvsappsdkv asprytltarifreemykellicgskssktpdgrtekpulkeplqqatfsyvll asprytltarifreemykellighthafpundkeplqqatfsyvll beflighthafpylganvokeylumtdagfalrepmkssaafinaievysapdelisd sgtalepylgeslyrepyliapotyrapavemanstitdgrtemippdsefynlikel vrttpsaikyepylterynytingktaisgldlstvagnlaapyykdivunatlmgpelqv queppergaikyepeyptlapotyvrapavemanstitdgrefydgrttgmgrefym fgarifgmgkagmyanafywm fgarifgmgkagmyanafywm grapetym greficigamykkwakenguwsuslidgefydgrttgmgrefym fgarifgmgkagmyanafym grapetym greficigamykkwakengum fgarifgmgkagmyanafym grapetym greficigamykkwakengum grapetym grapet	otation" -like protein kinase, ike protein kinase"	shiechemie, Am Niopierspitz 184, 1842. Martinsried, FKG, E-mali: schuelle@mips.biochem.mpg.de.mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk COMMENT Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/. FEATURES Location/Qualifiers 1. 89035 Source /organism="Arabidopsis thaliana" //variety="Columbia" //bb_xref="taxon:3702" /chromosome="4" misc_feature 1. 7016 /note="overlap to BAC F19H22; please refer to EMBL acc.	
/number=1 complement(11267. /gene="T22F8.30" /number=2 complement(12329. /gene="T22F8.40" /number=1 12329. 13974 /gene="T22F8.40" complement(join(123 /gene="T22F8.40" complement(join(123))	/protein_id="CAB43628.1" /protein_id="CAB43628.1" /db_xref="GI:4914425" /translation="MADIKDERGNPIYLTDAHGEPAQLMDEFGNAMHLTGVATTVPHL /translation="MADIKDERGNPIYLTDAHGEPAQLMDEFGNAMHLTGVATTVPHL KESSYTGPHPITAPYTTINTPHHAQPISVSHDPLQDHDLRWFGTSSTEENGBGVGRKT NITDETKSKLGVDKPSAATVTGSGSGSVHEKKGFFKKIKEKLSGHHNDL" exon	/gene="T22F8.30" 10875. 11536 /gene="T22F8.30" complement(join(1087511060,11267 /gene="T22F8.30" /note="similarity to dehydrin, Glycine /codon_start=1	/number=8 /omplement(9732. 98 /gene="T2F8.20" /number=7 /number=7 /number=7 /number=7 /number=7 /number=8 /number=9 /number=101041	<pre>intron</pre>	intron	ISTRSCPKLSQAYLYTTSPHLFSEEAEKAYSRVRDKVKVPLYGCDCYAYALLASGFVD

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AL035679
                                                      EU Arabidopsis sequencing, project. Direct Submission
                                                                                           Unpublished 2 (bases 1
                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SSMNTVFEQKENVSTESAAPSYLSPAQLSLSLASQPSSFPTSFLSSQSYLHPASSSTL
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16990. .17148,17278. .17407,17493. .17658,17826. .17908
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MSSSRSNKALSYDNYDNDCFGLQRDKLDHHGNRMSKHQOHTCGACSRPLSEKSLMSSQ
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Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich
E-mail: michael.bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosome
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27666. 27761)

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T76734 are in 3' untranslated region
EST T42894 covers intron in 5' untranslated region
strong similarity to ubiquitin fusion-degradation protein
- Mus musculus PID:g1654348

contains EST gb:AA395284, T42894"

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Arabidopsis thaliana DNA chromosome 4, contig fragment No.
                                                    3 (bases 1 to 55749; 38011 to 138479)
Murphy,G., Ridley,P., Hudson,S., Mewes,H.W.,
Mayer,K.F.X.
                                                                                           Unpublished 3 (bases 1
                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1. (bases 1133 to 1779)
     Ξ
                                     Unpublished
                                                                                                                           Zimmermann, W., Grueneisen, A., Wambutt, R., Smith, A., Mewes, H.W., Lemcke, K. and Mayer,
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                                                                                                                                                                                                  Robben,J., Braeken,M., Grymonprez,B., Volckaert,G.,
Lemcke,K. and Mayer,K.F.X.
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Pred. No. 2.9e-08;
0; Mismatches 16;
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16-MAR-2000 ment No. 90

Wohldmann, P.,

exon	exon	intron	exon	intron	exon	intron	exon	intron		exon									CDS	gene		gene		FEATURES source		COMMENT			TITLE JOURNAL
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gene intron	exon							C	מחה	gene	exon	intron		exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron
/ number = 1 complement(join(1116312361,1245512602)) /gene="AT4g38770" complement(1236212454) /number=1	. > 0 #	KKEVPPPVYKKPPPKVELPPPIPKKPCPPKKPKIEHPPVVYKPPPKIEKPPVVVIPKK YKPPPKIEHPPPVVHKLPKKPCPPKKVDPPVVHKPTKKPCPPKKVDPPVVVIPKK PPPKIVIPPKIEHPPPVVKPPPVKIEHPPIIYIPPIVKKPCPPPVPIIYKPPVVIPKK	FRAE SOURY LEDON WANDER Y LANDON LEDONG FRAE SOURY LEON WANDER Y LANDON LEDONG FRAE HOLD FRAE LEON LEON LEON LEON LEON LEON LEON LEO	/db_xref="G1:7270860" /translation="MRILPEPRGSVPCLLLLVSVLLSATLSLARVVEVVGYAESKIKT	/product="extensin-like protein" /protein_id="CAB80540.1"	H37643, T4252	)7 )6646, Z25647, T4	/gene="AT4438770" /forte="similarity to proline-rich protein, Solanum	19361 19455	/number=15 1116312602	/mumber-14 comptement(97299755) /gene="AT438760"	complement (96899728)	-	/number=13 complement(95819688)	complement(95399580)	<pre>complement(94849538) /gene="AT4938760" /pumbe=13</pre>	complement(91239483) /number=12	<pre>complement(90029122) /gene=*AT4g38760" /number=12</pre>	/number=11 complement(88299001) /number=11	complement(86938828) /gene="AT4938760"	/number=10 complement(83208692) /number=10	complement(81628319) /gene="AT4g38760"	/number=9 complement(80208161) /number=9	complement(78518019) /gene="AT4938760"	/number=8 complement(77697850) /number=8	complement(76707768) /gene="AT4g38760"	/number=/ complement(74957669)	complement(74177494) complement(74177494) /gene="AT4g38760"	complement(73357416) /number=6

COMMENT	REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS TITLE JOURNAL	RESULT 4 ATFIN2O/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Query Match Best Local Matches 6  Qy 1 cag		CDS	exon gene gene
lemcke@mips.biochem.mpg.de_mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.	Spermatophyta: Magnoliophyta: eudicoty; decided for core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  1 (bases 1 to 103270) Bevan, M., Wedler, H., Wambutt, R., Bancroft, I., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.  Unpublished  2 (bases 1 to 103270) EU Arabidopsis sequencing, project.  Direct Submission  Submitted (09-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martthsried, FRG, E-mail:	270 bp DNA PLN 10-MAR-2000 eliana DNA chromosome 4, BAC clone FlN20 (ESSA :2961335	ttch 44.2%; Score 54.4; DB 8; Length 198987; al Similarity 80.0%; Pred. No. 3e-08; 64; Conservative 0; Mismatches 16; Indels 0; Gaps 0; caggiatitytaaatgigagatgccttacaaccctgatgacctaatggcgcaatgcgagg 60	1811818224,1830218918,1904519298,1956419861, 1995420077,2017420415,2053420660,2073521189, 2127621580,2168121995,2215022418,2251823308, 2340423896,2399724387,2448024557,2464024753, 2490225183)) /gene="AT4938780" /note="strong similarity to splicing factor Prp8, Homo sapiens, AF092565 contains EST gb:T14115" /codon_start=1 /product="splicing factor-like protein" /protein_id="CAB80541.1" /db_xref="G1:7270861" /translation="MWNIDGTSLAPPGTDGSRMQTPSHPADHPSYTAPSNRNTPTVPT PEDAEAKLEKKARTWMQLNSKRYGDKRKFGFVETQKEDMPPEHVRKIIRRKHRLDKRV	.18918.1904519298.2956420415.2053420660.2973521995.2215022418.2251824387,2448024557,2464024387,71588216124,161917008.1718817661,17777.	ment(1245512602) "MT4938770" "AT74938780" "AT74938780" "AT74938780" "AT74938780" .16745,1684717008,1718817661,17777.
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                                                                  4 (bases 1 to 196247)
EU Arabidopsis sequencing, project.
Direct Submission
Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana DNA chromosome AL161556
              lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Camba
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich,
                                                                                                                                                                   Wedler, H., I
                                                                                                                                                                                                                            Unpublished
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Murphy,G., Ridley,P., Hudson,S.,
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                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 157343 to 167411)
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E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                   Robben, J.,
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GSIPTSPSGGNGGYLQSSVMAANFREFIEVVFQNWENSVQSWHVSGYSFFVVGMDGGQ
WTPGSRAKYNLRDAVSRSTVQVYPRAWTAIYIALDNVGMWNIRSENWARQYLGQQFYL
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VATSLNFRIQGHTMKLVEVEGSHTVQNIYTSLDIHLGQSYSVLVTANQAPQDYYIVIS
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QGILINGQfpGPHIDAITNDNIIISVfNYLKEPFLISWNGVQQRKNSWQDGVVGTTCP
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Pred. No. 6.5e-08;
0; Mismatches 16;
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		CDS	gene		exon	gene		exon	111 (1)	intron	exon		intron		exon		intron		exon		intron	CACI	0400	TUCION	3 + + + + + + + + + + + + + + + + + + +	exon		intron		exon		intron		exon	1111111	intron	exon		intron		exon	
tart=1	gb: N38012. AA713335. AI996517.1. AA71	complement(]oln(1231/126/5/1283412990/1309013199)) /gene="AT4g21830" /note="atrong similarity to CGT-131 protein. Homo saniens.	.12675,1283412990,13090		/gene="%14g2130" complement(1251712675)	1251713199	/gene="A14g21820" /number=15	/number=14 1173611823	/gene="AT4g21820"	/number=14 11625 11735	1146911624 /gene="AT4g21820"	7 :	1142611468	/gene="A14g21820" /number=13	111611425	/gene="AT4g21820"	/idimber=12	, a	/number=11 1087211094	1	/number=11 998310871	ļ.,	/number=10 9702 9982	90219701 /gene="AT4g21820"	er=10	94269620 /gene="AT4g21820"	er=9	92259425 /gene="AT4g21820"	1	9087 . 9224	/gene="AT4g21820" /numher=8		. 1	/number=7 86998879	1 .	/number=7	85448642 /gene="AT4g21820"	/number=6	83378543 /gence"AT4g21820"	/gene="AT4g21820" /number=6	/number=5 8220. 8336	/gene="AT4g21820"

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          Agrobiological Resources, Rice Genome Research Program; Kannondai Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2; Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                              Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA, clone:OJ1339_B08
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                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                   Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                      Published Only in DataBase (2001) In press: 2 (bases 1 to 119807)
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complement(15183.
/gene="AT4g21840"
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/protein_id="CAB79138.1"
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TKKFEEGTYSCAGCGTALYKSTTKFDSGCGWPAFFDAIPGAIKQTPEAGGRRMEITCA
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/gene="AT4g21840"
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/gene="AT4g21830"
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Direct Submission
Submitted (13-JUN-2000) Horticultural Science, North Carolina State Submitted (13-JUN-2000) Hall, Raleigh, NC 27695-7609, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Clouse, S.D. and Oh, M.-H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oh,M.-H., Torisky,R.S., Braam,J., Altmann,T. and Clouse,S.D. PHD Finger Dependent Binding of SHL1 to a Specific Promoter Region of Arabidopsis TCH4 in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF277453 1062 bp mRNA PLN 05-OCT-2000 Arb277453 1062 bp mRNA PLN 05-OCT-2000 CT-2000 Arb21) mRNA, complete cds.
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VHSFSSYTKLDSVGNDDFFCRFEYNSTTGAFDPDRVTVFCKCEMPYNPDDLMVQCEEC
SEWFHPSCIGTTIEEAKKPDNFYCEECSPQQQNLHNSNSTSNNRDAKVNGKRSLEVTK
                                                                                                     /codon_start=1
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/db_xref="G1:10644645"
/translation="MPKQKAPRKQLKSYKLKHINKSIQEGDAVLMRSSEPGKPSYVAR
                                   SKNKHTKRPG
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                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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/chromosome="7"
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                                                                                                                                                                                              /gene="SHL1"
                                                                                                                                                                                                                                                                      /note="similar to BAC clone F19H22 in GenBank Accession
Number AL035679"
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23815 c 24131 g
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               cactgactggt 74
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CTCTGATTGGT 609
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1 (bases 1 to 1058)
Speulman, E. and Salamini, F.
A bariety CDNA clone with homology to the DNA-binding domain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H. vul
X7757
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Zuechtungsforschung, Carl-von-Linne Weg 10,
Location/Qualifiers
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Plant Sci. 106, 91-98 (1995)
2 (bases 1 to 1058)
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ES43 gene.
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lgare (Dbg576)
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                                                                                                                                                                                                                          /protein_id="CAA54682.1"
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IECKCNVYSERDYTKLAAVNPEDYFCRFEYQSITGSEVPDRIAVFCKCEMPYNPDDLM
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/db_xref="taxon:4513"
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Direct Submission
Submitted (21-FEB-1998) to the DDBJ/EMBL/GenBank databases. Yasue Nemoto, Yokohama City University, Kihara Institute for Biological Research; Maioka, Totsuka, Yokohama 244-0813, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nemoto,Y., Kawakami,N. and Sasakuma,T. Isolation of novel early salt responding aestivum L.) by differential display Theor. Appl. Genet. 98, 673-678 (1999) 2 (bases 1 to 367)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachéophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                              thale cress.
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                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (E-mail:nemoto@yokohama-cu.ac.jp,
Fax:81-45-820-1901)
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260 from Patent
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76 c 96 g 91 t
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/note="salt-stress responding
/codon_start=2
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l. :217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="WESR4"
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                                                                                              GI:12311634
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AUTHORS
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                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problem such as compressions and repeats; all regions were covered by
                                                                                                                                                                                                    NOTICE: This sequence may not be the entire insert of this clone It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 80446)
Edwards, J., Wollam, C. and Dubbelde.
The sequence of A. thaliana T27D20
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                   MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-AUG-1998) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AF076274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 80446) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University Genome Sequencing Center The A. thaliana Genome Sequencing Project
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Preuss,D., Copenhaver,G.
                                                                                                                                                                                         neighboring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted by:
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8296 c
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                                                                                                                                                                                                                                                                                                                                                                                               Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63108, USA
e-mail: rwilson@watson.wustl.edu
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/db_xref="taxon:3702"
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thaliana BAC
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                     NEIGHBORING COSMID INFORMATION:
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78.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34.4; DB Pred. No. 0.31;
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C T27D20.
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                                                                          subclone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-1998
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                                                                                                                problems,
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                                   /gene="T27D20.4"
join(22634...227
                                                                                          PVSKFEAALEFLKLLR"
/gene="T27D20.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="T27D20.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:3702"
/clone="T27D20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .80446
                                     22705,22988. .23235,24132.
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The 3' clone is T24H24, 200 bp overlap. cosmid is at base position 1 of T27D20;
   Actual start of this actual end is at 80252 of
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Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation).

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organism="Arabidopsis thaliana"
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complement(join(12394. .12788,13045. .13861))
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IASNSVFHERTKHIEVDCHKVREQVQLGVILPHYTESEEQLVDVFTKGASTKVCEYIH NKLGVVDLTRP" FLSQRKYTLDLLAQVGKLGVKPAKTPLEDDYKAKRKGEHDNKPFEDATRYRRLVGNLV TWRSKKQKVVSLSSAEAEYRAMRKLTTELMWLKALLKDFGIDTPNPIPMHCDNQAAIH QKGIVVILVYVDDIIISGNDKVGIQDTKTFLKSVFDIKDLGELKYFLGIEVCRSKEGL GFTQTYGEDYLDTFAPVAKLHTFRVVLSLATNLEWDLWQMDVKNAFLQGELEEEVYMK PPPGLEVINAPNKVFKLKKAIYGLKQSPRAWYHKLSTTLMGRGFKTSEADNTLFTLPS

14338...18209 /gene="T27D20.5" /gene="T27D20.5" /gene="T27D20.5" 15011(14338...14992,14834...14890,14914...15492,15554...1. 16094...16517,16614...17066,17127...17229,17278...17578, 17636...17983,18077...18209)

/note="contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 19.54) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 12.35)"

IKLNTHGGLIRMLKNVRYVPNLRRNLISTGTLHSLGYKHEGGEGKLRFYKNGKTALCG
YLMNGLYILDGHTVATETCNARSAKNGTKLLIEKKEFKDLDFCEHYVPGKSKKLSFNV
GKHVTEDILGYVHADLMGSPNVTPSISGKQYFLSIIDDKSKKWLMFHKSKDETFDKF
CEWKELYENHYGKKVKFLRTDNGLEFCNNRFNDYCAKTGIERHRTCTYTPQQNGVTKR
MRTIMEKVRSPASAVDHNVPEQLMLNREPGYKHLRRFSSIAYVHQEQGKLKPRVLKG
VFLGYVPGGTKGYKVWLLDEEKCVISRNVYPEDDSVFNDLOSGDEDETVTQESQIEI
ETPPKSELETQNQVQGGATQYQLNDSEDEXNDVEGFAFALLVAREEVESEEVGFHDK
EDKDWEKWHGGMIEEMDSLLKNATWDLVDKPKNGKVISCHWLYKKKLGIPGVELPRYK
EDKDWEKHGGSIDXQEVESPVVKHTSIRILLSLAWKEDMDVKTAFLHGELD
ARLVARGFSHREGIDYQEVESPVVKHTSIRILLSLAWKEDMDVKTAFLHGELD
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VAKKBEKESEYEDDASDIKQATEEPDPIKFEQSEQAKNFIINHITDTVLLKVQHCKTA GAHFKLSSVHNDDERVGSEKVPYSSVVGSLMFMSKQGEVHWTAVKWLLRYLKWSIGLN LMYTKGFDFKVQGYCDSDHAADLDKNMSISGYVFTVGGNIVSWKSCLQPVVALSTTEA QTLFMEQPEGFEAPRQWNKRFNAFMMDQKFSRSVSDSCVYVKEVSNAKSMTEIKKLKK VLSREFEMKDMGAASRKLGIDIIRNRSEGTLCLSQTSYLERVIQKFRMDGAKVVNTPI EY IALTKAVKEAMWIRNLLDDMMLGTETAEVDIIEAGEVEVHKIHTTRNPADMLTKGI SSYIQLKHTLNTDVVSSAKSLERKLSETQESNKNVSMALYTTDRGRPQVRNQDKQGQG KNRGRSNSKTRVTCWFCKKEAHVKRDCFARKKKLENENRATMILLGDDHTVESRGCGT AE IWATLNKLFMETSCLNRIYTQLKLYSFKMVDTLSIDQNVDEFLRILADCLDQNLLP

.24348,24458. .24691

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EVHDLQIHMNKEHEVRSSSLYLSSKDVCKTMSAKGTVLLMVFKECLSTGIGDPELSAE
VQVVLHWYKDLFPEEIPPGLPPIHKGYIRESLSPCAVPVLLVPKKDGTWRMCLDCRAI
VQVVLHWYKDLFPEEIPPGLPPIHKGYIRESLSPCAVPVLLVPKKDGTWRMCLDCRAI
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/gene="T27D20.8"
complement(join(27921. .28322,28562.
/gene="T27D20.8"
/note="contains similarity to DNA
(cytosine-5-)-methyltransferases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENLGRTVADRRRKRFGPINTWGDMKYLLRLRMLSQGTRTVDEYFEEFEKLMNALELEE
SDEALMAQFIDGLQERIQRKVERAQYNGLHELLHLAVQVEQQIRRKASLSNRSRNNTP
WNASNNRAMDKSKVVESDHRFKNKSNEAPKTSRPKLGKFPSTNQSRSRYITCFKCQGR
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ENRSRAELLACEERMKKLEEGQSVMLHAARQEEKRKVRAQLTDPSSKYGTFYVQSDEV
EAANIRAAEVKVNRELLEEIEKGEIPSIAEELESVRADEIKFAQKAAEPKTPRPNPVE
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KAKQPQNEDDSGTRQKSSALSGKGPKISTSEARTSMKNTPDKEFYKRDADKKRKHSET
DARSBERSSRAGNEAKETGQNQOKGKNIKKGBSQDLVVLSSRYSBSRYSBGRTTSSPLB
PPMFFADTLRTLVHPRAIMPPLAELKATNREKLGEAVQEFNYAFLSHEDQLFEKDKEI
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CVLMRPSDAGKAPYVARVEKIEADARNNVKVHCRWYYCPEESHGGRRQLHGAKELFLS
DHEDVQSAHTIEGKCIVHTFKNYTRLENVGVEDYYCIFDYKAATGAFTPDRVAV"
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VETLMMKGIVSQAKKSGEQPPWIRDTLMKQMMVHWNTEDAQLKSETTSNCRNSDRGGL
GVHKHLAGQKSFVQVHQEMERLKRHVSYGEVFMQTHTRVDGSFVDQKSQHVGEAYVKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="contains similarity to reverse trancriptase (Pfam:
rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam:
zf-CCHC.hmm, score: 14.43)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41442.
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join(40097. .40331,40377. .40461,40515. .40592,40638. .41244)
/gene="T27D20.19"
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LNKRKRKESYASSSTSTVAQLQEQLQLKISEQEEQNAKLDEEHRQSQSRIASLEKLVL
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/protein_id="AAC28229.1"
/db_xref="GI:3377847"
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/protein_id="AAC28226.1"
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/db_xref="GI:3377845"
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/gene="T27D20.3"
                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 )oin(41442. .41817,41934. .42505)
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ATCHRIV11
LOCUS
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ACCESSION
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission

Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project lemcke@mips.biochem.mpg de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Coordinator: John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis
AL161499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/this fragment has an overlap with ATCHRIV10 at the 5' end and an overlap with ATCHRIV12 at the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory, John Innes Centre, Colney Lane, E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (bases 1 to 198022)
EU Arabidopsis sequencing, project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lamar,B., Stoneking,T.,
Mayer,K.F.X.
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Lemcke,K. and Mayer,K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                      /product="hypothetical protein"
/protein_id="CAB77865.1"
/db_xref="GI:7267153"
                                                                                                                       similarity to"
                                                                                                                                                                                                                                                                                                                                                     8288.
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TLRKEGLYANLKKCTECSDKEFEFDICVYDEYVNILLIIN"
complement(46940...49459)
/gene="T27D20.9"
                                                                                                                                                                                               /gene="AT4g03970"
                                                                                                                                                                                                                 join(8288. .8638,8738. .8949,8993. .9236,9341. .9454,
9527. .9676,10448. .10561,10690. .10770,10833. .10905,
10956. .11074,11199. .11279,11426. .11509,11626. .11679,
11793. .11986,12069. .12153,12238. .12735)
                                                                                                                                                                                                                                                                                                /gene="AT4g03970"
join(8288. .8638,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3702"
/chromosome="4"
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translation="MLADLDKFLSFPWGRESFLKTAVGMRPDKRNLGKSTGKRQLTTD/
                                                                                              /codon_start=1
                                                                                                                                                 (GB:X56794)
                                                                                                                                                                     /note≖"contains similarity to human CD44R1 gene product
                                                                                                                                                                                                                                                                                                                                                                            /number=
                                                                                                                                                                                                                                                                                                                                                                                              /gene="AT4g03970"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
/variety="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 to 28786; 28587 to 117434; 117235 to 197680) Stoneking, T., Stumpf, J., Mewes, H.W., Lemcke, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Mayer, K.F.X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA DNA PLN 16-MAR-2000 DNA chromosome 4, contig fragment No. 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34.4; DB Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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	exon	intron		exon		intron	exon		intron	exon		intron		exon	HICLOR	1	exon		intron		exon	Incron	1	exon		intron	•	exon		intron	(A)	2	intron									
3	/number=10 1142611509	1128011425 /gene="AT4g03970"	/yene- argoss/v /number=10	11199 . 11279 /genes "AT4603970"	ĭ Þ	/number=9 11075 11198	1095611074 /qene="AT4q03970"	/gene="AT4g03970" /number=8	/number=8 1090610955	1083310905 /gene="AT4g03970"	1 2	10771 10832	Ϋ́ P	/number=6 1069010770	/gene="AT4g03970"	/number=6	1044810561 /gene="AT4q03970"	/gene="AI4gU39/U" /number=5	9677 10447	7 (1)	/number=4 95279676	/gene="AT4g03970"	/number=4	93419454 /gene="AT4g03970"	/number=3	92379340 /gene="AT4g03970"	/number=3	89939236 /gene="AT4g03970"	/gene="AT4g03970" /number=2	/!umber=2 89508992	/gene="AT4g03970"	/number=1	86398737 /gene="AT4q03970"	₩ 3	NHLQGKLKSFKAAKMKSRVKWSEPMKQFIVGPNTEWFADIDTIYLPMIWDSKHWVGLA	SDSSPAREREKPTLSEAEVFLVAELLSKSKTGSYELLPSMSKSEFALFRNTLSAAPNT * EHLTSSGYLISNKFLLSLAKPTNWVSTLHMEVLVSLLSOKLATTLTNORAAFVOPWFA	DDTMKAMVIYSHDIHDTNSKPNKQLESSPTPTEDQITDSQDIGAHDLDENQEEGYYDV	KMQDSLDRETASHSHIDLPIDQSSEBQQAKIMSELIMVFKKDVNLMSEINFAAANNIY	VFGQPEVAQQVPDDHLDKTQDSSDSIPLINTEITDDPMDVFVTPLQSEHSNKDDANEG NPVYDTDVKDQNANEEDVDSQMQDASERVPTTHSGLDLPKEHNSEELETNANETDVDG	ELSNRVMKLEKAKKTVRFKRSTKLSSSFVACSSISKRKKIMEVPIQSQTSESHTLPEH	VISLPQIHALESNIKKLPVDPLIVGDLNADQSWAEWDDEVKDKKVAXWXDLIWVSHQFQ KTDWPGGDATILDTTSVDKKKOSBGHCGDRRYSTBSKDFINTSDDEKSBILTSET,OTKVE	PIKSIVSOLOOKTERLKGEPPALOLIAFRNIPGLLDLVLDDSTSKTILLWKRLTHPKO
Query Match			CDS	gene	gene		exon	intron		exon	11110101											CDS		exon		gene	misc_feature		exon	TUCTOR		exon		intron	!	exon	THETON	÷ ;	exon		intron	_
28.0%; Score 34.4; DB 8; Length 198022;			/yene- A.4903330 complement(join(3125631513,3171831843,3196432611))	complement(join(3125631513,3171831843,3196432611))	31256 . 32611 31256 . 32611 //conce"ATAC03990"	T 2	/number=2 28074. 28320	2795628073 /gene="AT4q03980"	/gene="AT4g03980" /number=2	/number=1 2705327955	/gene="AT4g03980"	GQSGHNKSTCVAAI"	THLVNLDKRTCTCCMFDIDKFPYAHGIASAKHINLNKNMFVDEFHSTYRWRQAYSESI HPNCDMEYWEIDTVSEVICLPPSTRVPSGRRKKKRIPSVWEHGRSOPKPKLHKCSRC	NSDKKLAQYLWEVDVRKWSRAYSPSNRYNIMTSNLAESVNALLKQNREYPIVCLFESI RSIMTRWFNERREESSOHPSAVTINVGKKMKASYDTSTRWLEVCOVNOEEFEVKGDTK	IASGLSENYPLAHHGLCTFHLQKNLETHFRGSSLIPVNYAASRVYTKTEFDSLFWKIT	FRKDHGVGINYSKAWRVQEHVVELARGLPDDSFEVLPRGYKLMRKVISIDGAHLTSKF	ADSLFIGKKFKDKDEMVFTLRMFAVKHSFEFHTVKSDLTRYVLHCIDENCSWRLRATK AGGSESYVIRKYVSHHSCDSSLRNVSHROAFARTLGRLISNHLEGGKLPLGDKOLIEI	/db_xrer="G1:/26/154" /translation="MFKVSFLFWQPRLTSRTIQACVSETSSIFDQQYSSSAFSTGLSD	/protein_id="CAB77866.1"	/codon_start=1	<pre>/note="similarity to similar to maize transposon MuDR mudra protein (GB:AL021710)"</pre>	, 1087, 556,		26352 26944 /gene="AT4g03980"	2	/note="pseudogene" 2635228320	20580 22438		/number=14 1223812735	121341223/ /gene="AT4g03970"		12069. 12153	/gene="AT4g03970" /number=13	1198712068	"AT4g03970"	/number=12 1179311986 ·	/gene="AT4g03970"	/number=12	1162611679 /gene="AT4g03970"	/number=11	1151011625 /app="AT4g03970"	/number=11

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (17-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk
On Jul 19, 2001 this sequence version replaced gi:13751315.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                   The true right end of clone RP11-212E4 is at 154195 in this sequence. The true left end of clone RP11-291I6 is at 133478 this sequence. The true right end of clone RP11-472K17 is at
                                                                                                                                                                                                                                                                                                                                               IMPORTANT: This sequence is not the entire insert of clone RP11-212E4 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13 constructed by the Sanger Centre Chromosome 13 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISSPROT; {\tt Tr:}, {\tt TREMBL}; {\tt Wp:}, {\tt WORMPEP}; {\tt Information} on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                  this sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   h://www.sanger.ac.uk/HGP/Chr13
-212E4 is from the library RPCI-11.1 constructed by the group
leter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                               //www.chori.org/bacpac/home.htm
                                                               1158
                                          /note="
                                                                                                                                                             /chromosome="13"
                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
'note="AluY repeat: matches 2.
                                                                                'note="AluSx repeat: matches 1.
                                                                                                                        clone_lib="RPCI-11.1"
                                                                                                                                         /clone="RP11-212E4"
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sequence from
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                                        L2 repeat: matches 2693.
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                                                                                                                    /note="1.
21668. .:
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21600. .2
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21593. .2
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21696.
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21609. .21992
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                                                                                                                                                                                                                                                                                                                                                                    /note="19 copies 22 mer 61% conserved"
21571. 21990
                                                                                                                                                                                                                                                                                                                                                                                                          /note="L2 repeat: matches 2490. .2708 of 21566. .21983
                                                                                                                                                                                                                                                                                                                                                   /note="14 copies 30 mer 63% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Tigger4(Zombi) repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="9 copies 4 mer atat 83% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="5 copies 33 mer 83% conserved"
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/note="AluSx repeat: matches 1.
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.14837
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.19872
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                                                           copies 60 mer
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                                                                                                                                  62; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="2 cor
5092"
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61468. .61770
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/note="34_copies 2 mer ca
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/evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                           'note="AluSg repeat: matches 1. .290 of consensus"
16788. .56865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="29 copies 4 mer caca 64% conserved"
19666. .49737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="11PB3 repeat: matches 6050. .6150 of consensus"
14551. .44586
'note="9 copies 4 mer tcat 86% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="L1MC4 repeat: matches 7670. .7974 of consensus"
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26684. .26812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Tandem repeat. Forced join. Assembly confirmed
                                                                                                                                                                                                                                                                                                   'note="L2 repeat: matches 2605. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                      'note="THE1C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="17 copies 4 mer cctt 67% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="AluJo repeat: matches 121. .276 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                  note="HY3 repeat: matches 1. .78 of consensus"
                                                                                                                                                    27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e="MLT2CB repeat: matches 1. .495 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3. .50998
e="L2 repeat: matches 2592. .2671 of consensus"
3. .51968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4. .33941
e="24 copies 2 mer at 75% conserved"
6. .37970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e-"MIR repeat: matches 123. .211 of consensus"
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                                                                                                                             0;
                                                                                                                             Score 33.8; DB Pred. No. 0.54; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 repeat: matches 58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matches 3. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matches 6128.
                                                                                                                                                                        DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (08-FEB-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://mgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924) on May 31, 2000 this sequence version replaced g1:6997824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Only in DataBase (2000) In press 2 (bases 1 to 166266). Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 166266)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 166,266 genomic DNA of 11q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP001146.2 GI:8118522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguencing vector: PCR products; 100% of reads Seguencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 155729 bases at least Q40 Consensus quality: 160730 bases at least Q30 Consensus quality: 162836 bases at least Q20 Insert size: 164766; sum-of-contigs Quality coverage: 5.73x in Q20 bases; sum-of-contigs
                                                                                                                             94309
107839
117166
124148
131541
138929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: Humbraft11
Center clone name: RP11-727G17
                                                                            144192
151056
                            156286
159077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
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sapiens DNA, clone:RP11-727G17.
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                                                     158976
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map 11q22, WORKING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156186 156285; gap of 100 bp 156286 158976; contig of 2691 bp 158977 159076; gap of 100 bp 158977 152099; contig of 3023 bp
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162200 165096: contig of 2897
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43658 43757: gap of 100 bp
43758 60093: contig of 16336 bp in length
60094 60193: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
43758. .60093
                                                                                144192
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124148. .131440
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117166. .124047
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/chromosome="11"
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                                                      note="assembly_fragment"
                                                                                             'note="assembly_fragment'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP11-727G17"
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117065: cc-
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1055
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166266: contig of 1070
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156185: contig of
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'513: gap of 100 bp

94208: contig of 16695 bp in length

308: gap of 100 bp

1007738: contig of 13430 bp in length
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contig of 9227 bp in length
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COMMENT
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ORGANISM
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                                                                                                                                                                                                                                                 O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                               All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                    Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7331563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Maddonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
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Birren, B., Linton, L.,
                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center
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37047 c 36491 g 44059
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159077. .162099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185404 bp
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56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .165096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_end:SP6 vector_side:left"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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for Genome Research

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 55 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9431: contig of 9433 bp in le
9434 9533: gap of 100 bp
9534 10744: contig of 1211 bp in le
10745 10844: gap of 100 bp
10845 12149: contig of 1305 bp in le
12150 12249: gap of 100 bp
12250 13273: contig of 1024 bp in le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 3.8
Quality coverage: 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: 30 Center clone name: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 0.960731
Consensus quality: 158038 bases at least Q40
Consensus quality: 173087 bases at least Q30
Consensus quality: 177952 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 157000; agarose-fp Insert size: 180004; sum-of-contigs. Quality coverage: 3.8 in Q20 bases; Quality coverage: 3.3 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-terminator Big Dye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        soon as it is available and the accession number
                                                                                                                       7853 27853: contig of 1520 bp in length
7854 27953: gap of 100 bp
7954 29293: contig of 1340 bp in length
795 29393: gap of 100 bp
795 54004: gap of 100 bp
795 55149: contig of 145 bp in length
79 55249: gap of 100 bp
8 56517: contig of 1145 bp in length
8 56517: gap of 100 bp
1 57905: contig of 1188 bp in length
8 56517: gap of 100 bp
1 59297: contig of 1388 bp in length
59397: gap of 100 bp
1 59397: gap of 100 bp
            100 bp 62491: contig of 1608 bp in 1. 52591: gap of 100 bp 64008: contig of 1417 bp in 164108: gap of 100 bc 4108: gap of 100 bc 468282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1373: gap of 10
652: contig of 10
652: gap of 10
15679: contig of 10
7779: gap of 10
16942: gap of 10
  08: gap of 100 bp 65352: contig of 1244 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                   24920: contig of 1272 bp in length
100: gap of 100 bp
26233: contig of 1213 bp in length
133: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72: gap of 100 bp
22260: contig of 1188 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project Information
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: gap of 100 bp

972: contig of 1005 bp

: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of 100 bp
18: contig of 1188 bp in length
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gap of 100 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
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1005 bp in ?
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f 1305 bp in length
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163 bp in
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179 bp in
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/e; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sum-of-contigs
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                                          length
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  misc_feature
                                                                                misc_feature
                                                                                                                                                                                                                               source
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81092 81191: gap of 100 bp

81192 83043: contig of 1852 b

83044 83143: gap of 100 bp

83144 85037: contig of 1894 b

85038 85137: gap of 100 bp
                                                                                                                                                                                                                                                                                                              169230 169329:
169330 18511
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156704 1692
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vector_side:left"
9534. .10744
                                          clone_end:SP6
                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                /clone="RP11-304I11"
/clone_lib="RPCI-11 Human
1. .9433
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                           note="assembly_fragment
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66782: contig of 1330 bp
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5480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5480: gap of 100 b
119514: contig of 4034
                                                                                                                                                                                                                                                                                                              9329: gap of
185113: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90847: contig of 1474 bp in
947: gap of 100 bp
93191: contig of 2244 bp in
291: gap of 100 bp
291: gap of 2703 bp in
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70756: contig of 2261
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gap of 100 b
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contig of 7972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ap of 100 bp
contig of 3405 bp
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                                                                                                                                                                                                                                                                                                          of 100 bp contig of 15784 bp in length
                                                                                                                                                                                                                                                                                                                                                  contig of 12526
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100 bp
- 7244 bp in ?
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10432 bp in
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1843 bp in
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                                                                                                                                                                                                                                    Consensus quality: 242878 bases at least Q40
Consensus quality: 257347 bases at least Q20
Consensus quality: 260576 bases at least Q20
Estimated insert size: 250000; pulse field gel estimation
Estimated insert size: 250000; pulse field gel estimation
Quality coverage: 4.84 in Q20 bases; pulse field gel estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 32 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* to the gaps between them are based on estimates that have
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On Feb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (30-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 14, 2001 this sequence version replaced gi:9256699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Project Information
Center Project Name: 85939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 265815)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
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provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available
the accession number will be preserved.

1 1204: contig of 1204 bp in length
1205 1304: gap of unknown length
1305 37886: contig of 36582 bp in length
37887 37986: gap of unknown length
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10845. .12149
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WORKING DRAFT SEQUENCE,
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/clone_lib="CalTech human BAC library B"
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/db_xref="taxon:9606"
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219091: gap of
238513: contig
238613: gap of
242453: contig
                                 25.7%;
55.5%;
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265815: contig
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7247: contig
72347: gap of
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92274: gap of
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g of 12481 bp in
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                                                                                                                           62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Newsome, A. L., McLean, J.W. and Lively, M.O.
Molecular cloning of a cDNA encoding the glycoprotein of hen
oviduct microsomal signal peptidase
Biochem. J. 282 (Pt 2), 447-452 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission Submitted (05-JUL-1991) M.O. Lively,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1. (bases 1 to 799)
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/translation="mntvlsranslfafslsvmaaltfgcfittafkersvpvsiavs
/translation="mntvlsranslfafslsvmaaltfgcfittafkersvpvsiavs
rvtlrnvedftgprersdlafvtfditadlosifdmnvkolflylsaeystknnalno
vvlmdkiilrgdnprlflkdmkskyfffddgnglkgnrnvtltlsmnvvpnagllplv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="oviduct"
/cell_type="tubular gland
/clone_lib="lambda gt11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Gallus gallus"
/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                           /product="microsomal signal
/protein_id="CAA43208.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-MAR-2000) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B. Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J. McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RPSSLALVPYSRPLSSETVCFFSKHCGYNALDLIEKVILSATSSIVLKNVVPSSKSLA
QALILKALQGVPVSIHCPHKTLKALGDLSKQTNVTLYSSHASSDKQTLIVDEHQVVTG
ARNFTTTSLHREANLMRISSLDLANLLEKNOKGEVCLGQQKVCYCPISKNKKGGNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="synonym: Chlamydia complement(136. .1230) /gene="TC0435"
                                                                                                                                                                                                                                similarity; putative"
                                                                                                                                                                                                                                                                                                    complement (1247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GP:2444077; identified
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(136.
/gene="TC0435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE002160
TYSDLSKTTIELIQFQENSHALLHNKTLIIDKQQIITGNGNFTSASLCEDVNLMMRIN
NMHLASLMEKNQAGRACIKKQKVRYLPVNRKGEIVKEIQKASSSIQLGMYILTNEAII
                                                                                                                                                                                                                                                                                                                                                   complement(1247.
                                                                                                                                                                                                                                                                                                                                                                              DLCTWWRSLCDSSTAITYEEAENADSSSSE"
                                                                                                                                                                                                                                                                                                                                                                                               EILKEIQKATSSIQLGTSCLTSQSIILALDEAVTRSVIVTVIIDSNNKQYTLEKLSSL
CTKINIRVGTRSSSNCQVCIVDHTTAIIGCSSNRPTRRQNANQEAVLIISPLTECQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="phospholipase D family protein"
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/db_xref="GI:7190478"
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                                                                                                                                                                                       /transl
                                                                                                                                                                                                                                                                              /gene="TC0436"
                                                                                                                                                                                                                                                                                                                             /gene="TC0436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MVSPLITTTSPYLLTLQARLLFTLTTSCSSQNQKTCAKKIQELT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:83560"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                            /codon_start=
                                                                                                                                                                                                                                                        note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             muridarum
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                                                                                                                                                                                       _table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                section 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shen, C., Gill, S.R., Heidelberg, J.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                       .2431)
                                                                                                                                                                                                                                                                                                                                                     .2431)
                                                                                                                                                                                                                                                      GB:AE001363; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
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gene CDS

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/gene="TC0438"
13043. .23050
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NSFWPDELPTIPKGDYRTVILGYGTTYEAVTEVVYLSNKYWREAVMESSSRYYRPPL
TAKSKLSTIIGGDSPLTVIPVRLIEKDEKENLDHAASYKDYKINIKGKGCLTVOIGG
AGEYNLTGTLPATNTISFRAIPAPFGVKFNLSLVEQDVPLIRPNGTEEKFLKIRQTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMSFCVENGVESDHTMISIAPGFFNGASYSMOHYLSALYEIHRHILGSLTSDLIKKE
LESKGAGCFVHEERFDSLLKASSEKQYLSLTEIHKSLSKQTHANTALPGV
GKIIEREGDFGRLGITTTETSVAMRSVDYRGIGVSKDLFSLPOEVFTLORVVEDAKY
GKIIEREGDFGRLGITTTETSVAMRSVDYRGIGVSKDLFSLPOEVFTLORVVEDAKY
LLSWFBFYNRYANAWSDLATHYGAEILEAHPQSFLYEVEGRCMGLSLLYMSIEDEGGY
RTLQGNLDTVSALYQQKERDHLFLSSKOQSLLSKDLSLLNWCZYGGNKVLLENRGFNA
KWDVLQLTGTFEKSLTKSLLITTFHSLTLNFWGSFFFXVTDRWFGHPPPSLAAALY
KWDVLQLTGTFEKSLTKSLLTTTFHSLTLNFWGSFFFXTDAPEGHDPFSLAAALY
FIEDMVQVSPHIKQRYGFSETLSVREQLQVXFLDAPEGIQSLLSFTDAGLLSSHQATT
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TGPDLLVDEMKTY FRSLGPIGKDYLEGKKLGNKAFLGSYNKI VEGKOTTDWLHPVTV
GANDVTPADESTWCGIKORCLAELFSDESKFRPETPKGISRTXIDKYFTFKLMSROS
GANDVTPADESTWCGIKORCLAELFSDESKFRPETPKGISRTXIDKYFTFKLMSROS
GANDVTPADESTWCGIKORCLAELFSDESKFRPETPKGISRTXIDKYFTFKLMSROS
ELFLRGTSFP LANGULNVENGLFTFDLIKFTDVDRALYVLRNQVCDDASASAAVFSLQLQLA
ELLRGTSFP IANGULNVEPDLNRNIASSLEKTIKLYLGSISQTETVIMHSAISDRYMFL
RDMLATABEMRLVKESIFKKETFPLTTEEIKLLNSWAELOSKONLGILSLEEVDKLD
UTSSIMENSKLKKRVAAIEDSIVAGYFYLRLEETLSEMVRIPREDKDLKKRVIRFMEGMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                VSDTSLKLENFVRYLMEAETIELYRQLLYAQNLLRIHNRDLVLKLFYVRQSEGMGAVL
ITFKNFFIESMEGISAPTLEREAKPILASDPMGLINPAYREHLDLFLGEDKLNLAILV
QEFSMLQYIVSMQEGKALGSLLTPPRYXDMNLAVLTYTVASSWEGRREASWLKAPIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVLENGTAKFITNRKHIVYSÞKÞYSELAVTQSRDIKAFVQGNTGCSYVFSTIYRSSQK
TQQTELTLVDDDVYAQTIDVSSILÞTLILAKKSGDNQIDFEFSSSHHLMAIRVSWKGV
IÞERTRVKINNETILRLGWLNAKLMASRNÞSYWNLLYVNRNVIÞERVEDVKSLNNTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTILGSSEGNDTLTGGNDTKFYSSPGGGTIYSGKGKVEYHIPQLTHPLHIILSKGSSA
HQLVTEINADQVKPVLGSLSLTSSMELISKQEIHVSSEDTKEDLGVWKERYEVRLGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLETALGAWNLYDSVVSLKEAQTHSDRMAARVDIAFNSITLGITIASVALPSLMLAVG
PLAAIGMGASAIARNVALKEERYDQWLVYKKFLTEGGSHILFADPDRHLLDFSGNYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FKQFSAKANELGATGVMDLELGMSIVSIVQYMRLLEEGKGKDPLAVANLVMDVKETAE
MTVGAVIQGLSKKFITQEGVDGFRLETAIASQLKKASSRVGGSVGKVFSKTAAVLELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEKMRERGPVIIERIQTTWGKLYEIGGSIHHRRIDEFTSETDLDEMKLNGDVLTDFLT
KHVLDSETVSLILVLLETRGLEEGTKHVSRSLIVETPDEAASLFQFLKNKTAKTREML
VSLLSEVTDKLKSAQLDGEDVEVSRVSFSDNSDEITVEVKKGSLLKKLSIRGGGIFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANQQHPDERGGRWYSQLYDESFKKRVTAPVKKIQELAKKYLNEQRVHVLEIDDYLTKN
PLFNRLHEEGYAFSDLTEITRYMLAEYGISGIFSEGNILPSPSARLVNIIKTYYGGDY
HDWQDVLPKIYDWLASGGAADLTNERFAAIPESLRKNLEGLHGTDLLTPPVDASVSGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQQYKDLIKANEQKIKDIVGKVNTDLGKERVFIKNIRDLSSMQDRTNTYNYEMEMLLR
WNYPASADQIRWMLKELGGIYTDLDMWFQYSPDVLQMINETGGGRFFEELFIRRAYS
DGVLEALANGESGITIONIAQDIDISKLTRSDRTQLEKLLTDIENKQKSSGTSKFESLG
RMAPDSVRDFMPILQRHHKWSTGWNVRGLNGLMMAHKGSAMVDAVIKGQRQAYRELKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFSLNTVPAKIIHHENGTKQNWESKQPTVSSEKSSNKRDVSESIAVVQRVNPEVITKS
SLKATKSIRRRKPRSVEEKREQLVKDPADKIVYDLRADTIASRLKLTEEQIQKCRISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVIIGSANWSNRGLNTNKEDLLIISPLTEGQKQDLCTWWHFLCENSTVLAEETKTPKI
LD"
                                                                                                                                                        RVLKANKNVITIPMKSSYTKK"
                                                                                                                                                                                                                                                              PNVINNAITYYRVVVPFWIRNRLTKGSLIRIPAHSIPIALTTTQNDVFKTIYAPGFSI
                                                                                                                                                                                                                                                                                                                                                    KLPLETTLTASYYLXPYSGDLYVTCLMNRRPQNQAFVIRFKGYKFQKGAFRSIALISS
HSYGESRIAKTVLQFRGQELFHLEKSAPNKSAVLQLDSKLLSLSRMLFYGGDQVIRYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVPAHKTKYLFFTDEESLANPEDNVLFYSKLGSNTLQASQKPLTQFARQLWASYDEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>LMPPNTKRNGEHVFAIENQEGVDVKVLGFLQSGHVLGEYEEDLMYKDVFARKITHFAV</u>
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                                                                                                                     13043.
                                                                                                                                                                                                      YFSFLGLDAFLKPRTHNRVGDMLLELEKEVVVTVKKVDETDYNKKRVYIVTELTKEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITATPIDQMNAGTRLVTMGVKTCDVAKWQKQHPTETSYPEDILDWLTQKSWFLAPEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YKHLSQEIRTNFDALFLKNMVLSQDGFFNYCLLKGIGTIDDQTRIAYLQDELHLPEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILKKIAFDSSLKELRSITSQETQDFVKEYDELQAKYQTSGRREERRELEKDLRKLFDR
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/db_xref="GI:7190480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3255. .13022
/gene="TC0437"
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                                                                                                               .23050
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WARYMEAIFELQOKIVNGELQTVETVKNILQKKGAESLYHADRAALLVQFSELRYHLS
LTEVQKCLADLDNLGQAPSYLLTGPLF6CIGH IMLRDROFGLFLATSWTDPIGLSTYDF
GGIGGKDVFSTPSEVPSIHTILDRVKYDTFSWKKYYEKYSGIMGDLAFRLGAESLRI
HPQTFIYDTEGKCMGLSYLFLAAENILAAYGILQDNLSTLSALFLEREREKLFLSREDN
RFLDRGLALIEWLQHRGNSELQAGGIFSTVDWDIPSLTKLFEKSSVPGVLVTTPSHAV
TLHFFDCAFRYTDPNFGHVDFPSLESALYFLEXWQISSDVRAQYGIKEGVSVPQQLK
VYVPDSIEARNANNIFTDAGLVTGYQATTLDRWIYNGEASGIRTTWATLFAWGUTL
NGNRIDERTKESDLDKTGINGDLTTSFLSKNVLDERGVALGRTLVETLPFVAGTRLVS
SGAIVETPNDVASLLQASRERLSHFKDVIQVLLRELATKIHGKGLKDSDKVSVKSVTV
EPSGEAAIVLEKQDTPKKTSSTISVKIKLBAFQNFGKSLMELANTGVNAVELGLS
SGAIVETPNDVASLLQASRERLSHFKDVIQVLLRELATKIHGKGLKDSDKVSVKSVTV
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RVAIYNLLNPEEAAKARKALEKKERDKKGKQQEKDSSEGEDQGGOKKNFSEYAELLK
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QYEQHRAKDSLGLLSEREQMTFLEITTQIAENFTLFSVISGEBEISGSVYFRALESO
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GIFSSRAIFPADSKGLVDLLKKTLGGDFATLODALFTVYDWILEEPNSERTNKLFKGIF
PENLOKELKNIAPEHLLTPPIDTSVSALGMRFSTEVGLESDSVMASIGSGFFNPSSYS
GVENRDSINRKVHGQLYAGFITHTIENRHWYTLQPNLVEFDITVPAKSIKYFVFRGRL
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MYAQNLAYIYGRDFVLKFFFIRSGTGIGAIQLVFKDLFKDSFGTEKTLGKEAKSTTPL
                                                                                                                                                                RGEGNNNSGIFVSNFDASPSFEQWVNKFTVKMADGITLFALNKSSEDQNFSLATTNTI
VTLGYHSVDOTIWSNRLPEEPSYIENLENWLKKFCWWLAPKVTYVLQREGTADFYYRDQ
KLIYHPKPFAELDLHPQPGYHTYVNGSIGDTYIFSESPWVLSTYKLSLADDLGHSQT
VDLSSLVPTFVRGRMTSQTVNGPSIDLEISSPRYTFLPLQISWGSHVLPRNTRFDVMPH
HSPTLGEWYDKLNTNTSEWHTLFHNSMLIPKSLVSVLSLNNTVTVMVRHLERKNEHIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLSLIQYARLYDAGKGSSPEALFNLILDVKELTEMTVGTVIQALQKQFITPAGIDGFR
TETLLARQIQKVGTRVGGTVGKALGSVARVLELPVLETIAGVWGLVSSVEDLLHADSY
SDRVAAKVQISFDVITLALTLSSALAPLAMLAVGPIAAIGMGAASIARNVARKEERHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WGPLGRDFLTPRGKKLGDMAFLGSYKKIPLDPSDPRKYTFDWMNPLTVGSNDVTPADE
STWCGSKKRCVAELLFSDSSTKLSTNKLQGVTRTKIDTSTFTSLWKEESKKKLPPGLL
ESFNRFITEKTVDILKLSELDQKIYVTQSAIQDDNIAKASLFSLQLQLAHLLRFAPYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DMMPAFSQEVLEVIKKHSVGDRMFEDMTSRRAISDAVLKLAVGETTTVSIEDIGKDID
ISRLTEEDKTKLGELFKELEFFVKKDTQNSSKLGKAKSFFQPMNMDIVRDTMPILRRY
HYYPELGWFVRGLNGLMVSHKGSAAVSHVIKGQQDAYQELAAMRQEVLSGEFFRSLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSGGGKIFSGLGKNWYHIPKLKGRLDIILAKNSAEHLLLMDDYSYNWQSLGTNLTLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQYKVYTEIVYLSNQVAWRDAVMDPTSRYYIPPLVEEGKSATIIAGNTPLNVIMLRLL
DEDTPARISQNLAYKDYKIKLVGGKGGLTVQIGGGGTYTLTGDVSAKNTISFRAIPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AWVEYKQFLDSAAKLVVKAYPESHLLDLSGNRVLGNLYLDLSQNPPLLKGDVSRNYDS
LIGHVGDWSDRQVRNRLGYGYRSSPERALAKGHANTRWPREIPHIAKGVYETVYLGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDLKKKYEQRIAQTHSTKKKNEYLQDLQSLLEKYKTVSDEVRGRFDVLFLKNVVITQD
NFFNYCLLKGVGNISDETRMEYLEKELKFSKEEIEEYRKLKESNKEKIASVVKKLNEQ
LGSARVHIKDIKELNSMKHSQNIYNYEMEMFLRWNYAAATDQVRMYMLEEYGGLYTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAF39292.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGVCFNLSNHAMQNVPMMRPNGTKIEALKIQQTGFSVIAGSAEGYDILTGEKDTHFYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTHRQHKDLIGGHLVSDYLAKSLFFDYRQDSIMPEAVSTLGITGPDLVAQKLVELFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRVFLDTYPDYSFYFWVDSNAYGAAKFSGILKRMAFDVAIQELRDSTEESTKVFVKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSDKKGNEKKTEEKSKVSFIKDVADIIKAEFSGHLVPVDKIIHGIWIAGAPPEGIEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mpvsgsivaskentsaslqpattlnngssveffqqitvyddarn
ftnHttedvikigeqlqrkfynmtegtqvpfttspayhtgnwktafiynlaqvianlf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLGLSSEQQTSVKELLNKLRKAITNYNALIEKNSSEGQSLLIRQAKLVEEIQEKISPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNIHNHTPDKKSSGESLRNISLEKPVLSRKRRDVEKNKEIKNEPSVNKYDLTYKNIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSTIQPIRVNSTRSSPFSTNSSVEKRNRFTSKDTKVQPPHTTRSVSPRKRKSVIVTRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GP:6013469; identified by sequence
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                                                           Query Match
Best Local
                                                     Matches
  9578
                           9518
                          70
CTGGCAAATTCGAGATAGAATAGGTTACGGTTATCGAATTTCTCCGAC 9625
        60;
                                                          Similarity
                                                     Conservative
                                                           25.4%;
                                                     0;
                                                          Score 31.2;
Pred. No. 4;
                                                     Mismatches
                                                                  DB
                                                     48;
                                                                 μ
;
                                                                  Length 23366;
                                                     Indels
                                                    0;
                                                    Gaps
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0;

CDS

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FEATURES
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
REMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-JUN-1996) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RO, England and Department of Genetics, Washington University, St. Louis, Mo 63110, USA. E-mail: jes@@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
Rhabditoidea; Rhabditidae; Pel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The true left end of clone K10D6 is at 1 in this sequence. The true left end of clone T19B10 is at 30388 in this sequence. The start of this sequence (1. 108) overlaps with the end of sequence ALD21173. The end of this sequence (30388. .30494) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTIANT: This sequence is not the entire insert of clone K10D6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the nematode C. elegans: a investigating biology. The C. elegans Sequenci Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neighbouring submissions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            none
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans cosmid K10D6, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence Z74043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 30494)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 30494)
                                                                                                                                                                                                                                                                                                                                                                                                       /gene="K10D6.1"
join(1925 ~~~
                                                                                                                                                                                                                                 Similarity to Drosphila GABA receptor beta subunit (SW:GAB_DROME), contains similarity to Pfam domain: PF00065 (Neurotransmitter-gated ion-channel), Score=148.6,
                      /translation="MLQIFLINISISFPLVIFSFIFQLLSMTLFLPNWCSGFYYHDDV
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                                                                                                                                                                                                          E-value=5.7e-43, N=2"
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                                                                                                                                                                                                                                                                                                                                               /gene="K10D6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="K10D6"
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/db_xref="taxon:6239"
                                                                                                        /db_xref="SPTREMBL:Q21420"
                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                                                                                                                        /note="predicted using Genefinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:1403245
                                                                                                                                                                                                                                                                                                                                                                     ln(1925. .2071,3486. .3705,3814. .3893,3953. .4045,
38. .4174,4480. .4528,4580. .4905,4954. .5404,5462. .5539)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n(1925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30494 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                       925. .2071,3486. .3705,3814. .3893,3953. .4045,
.4174,4480. .4528,4580. .4905,4954. .5404,5462.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromadorea; Rhabditida;
loderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sep
                                               gene
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                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
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.23550,23983. .24056,2 02,27954. .28159,28296.

.24056,27146.

.27301,27401. .27463

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/note="predicted using Genefinder"

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/gene="K10D6.2c"

/codon\_start=

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```
complement(join(6150. .6262,6410. .65
6977. .7187,7236. .7461,7969. .8202))
/gene="K10D6.2a"
                                                                                                                                                                                   EHQHGLMWDCIRAEKHVVSVGDFYDETPLHCMYKFDNSAELVIQNTLNNIDEDGAAGE
SEHHREMAWHKALIFFIITSEFLAFISICSGVCAPCVBSTAFASISLEIAMLCSLLA
DGIFFLAANRYDNRFVGAMVGTYGARTGYAFYLHLMGTLCWIGAFVCTHLTTYKFVTG
DEEDGSKENLFTWQQQTQPVTLSVLCVCFVFCWCASLSFQKIRRSSSAATTVSSQQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(6150. .6262,6410. .6594,6777.
6977. .7187,7236. .7461,7969. .8202))
/gene="K10D6.2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGIFFLAANRYDNRFYQGMYGTYEQRIGYAFYLHLMGTLCWIGAFYCTLLTTYKFYTG
DEEDGSKENLFTWQQQTQPVTLSVNELPYRREEPLLHDKFYSSQQAGYRPNPQVPYRT
TSITQYRETSA"
complement join (6262, 6406.
                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA98514.2"
/db_xref="GI:6425186"
/db_xref="SPTREMBL:045670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA EST yk255d4.5 comes from this gene cDNA EST yk526b2.3 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:045669"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="cDNA EST yk284g4.3 comes from this cDNA EST yk284g4.5 comes from this gene cDNA EST yk525b5.3 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSLGTKAMPARTMLGVNALLAMIFQFGNIMRNLPRVSYVKAIDVWMLVSMTFIFLSLL
ELAIVGYKTNNEEGSKKKCPHKKLLDNFEASPAGLCRYEKRFMLPVERRSARWGGIIR
EQVFQDFWNWSPEKIDRVSAIMFPACFAIFNIYVSYYNKKLEKAEMKLNEDRL"
                         /gene="K10D6
                                                                                            complement(join(6262,6406.
                                                                                                                                                      NVDQLIFNFFITFFLSLCFESTHPSSIKMSFHTEERSHCSTTNLYHHNKPAIGRTHRF
                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEHHREWAWHKAILFFIITSEFLAFISICSGVCAPCVPSTAFAFSISLFIAMLCSLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA98513.1"
/db_xref="GI:3878481"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(6124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7236. .7461,7969. .8202))
/gene="K10D6.2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WVNYRVNVKGPCDLSLELFPLDIQECHLIYESFNYNNQEVRMRWNEKSAEPVSVTNKI
RLPDFELIKIESTRISAPYPAGMWDELHVKLVFERRYIWYFMQAYLPTYLTIFISWIS
                                                                                                                                                                                                                                                                                                                /translation="MGSTVTQKLLLALSIVLILVGICLTSAGCFSPAWQVVDIREFRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="cDNA EST yk255d4.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="K10D6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .7461,7969. .8202))
="K10D6.2b"
                                      . 2c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comes from this gene comes from this gene"
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      .6594,6977. .7187,7236. .7461,
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 tattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgc 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTGAACGGGAAGATTTATGTCCAAAGTAAGACTCATTTTTCATACTTTCCTCGGAACA 19719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTTTCAATCCAAATGCTCTTGGAATCTTTCTCACTAGTTCTCGGCTTGTAAAGTATGT 19660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               actgactggtaagtttcacatgtaaggtgatacttatcttcaatttattccacacaaca 123
1 (bases 1 to 83145)
Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., Vanaken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H.,
                                                                                                                                                                                                                                                                                                                                   complete sequence. Sequence
AC002339 AE002093
AC002339.2 GI:6598350
                                                                                                                                                                                                                                                                                                                                                                                       AC002339 83145 bp DNA PLN 05-APR-2000 Arabidopsis thaliana chromosome II section 226 of 255 of the complete sequence. Sequence from clones T32G6, T11A7.
                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                  thale cress.
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GOKFAQLNEKVMISHIVRNFKIEPTLKYNDTKPCLEVVTKPSNGIPVRLIRRN"
a 5582 c 5196 g 10100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGNLGPIVGKKTEDLPSVFINWAAEQRDQGHSVMRVMILGKVYAWPLNGKAAAAIIDS
TTETNKGDDYRFFDPWLGGGLLLEGYGERWKSHRKMLTPAFHFAKLGGYFEVFNNESK
LLIDLLSDFSASGETVDIFPYVKRCALDIISETAMGIKIDAQINHDHKYVQAVEGYNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Join(29944. .30048,30200. .30266,30347. .30494,
Z74043.1:108. .267,Z74043.1:318. .1008,Z74043.1:1324.
/gene="T19810.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TETVLEPCEGXVDMTVEKGNVEXSFAFFYYNPTICDPTPEDAEMPMITDLSPVV"

JOIN(2944. 30048,30200. 30266,30347. 30494,

Z74043.1:108. 267,Z74043.1:318. 1008,Z74043.1:1324. ...

/gene="T19810.1"
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SSSSFTISSSTRPSGSKGFMIMPAELFDHVDSHLSYEDSNNFKSAHPLIDIRLTSNL
IYYDKLHLSDDEDDCWISDTRGRVVPRRFNANNASDLFRSLENLKEVTVIMKDVNVKN
LQAMGPQNNFTECTPYTPGGYLQKLFGGISPSELHLRQLSLHVDIMVESLEVYCLVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="K10D6.4"
/note="cDNA EST EMBL:T01379 comes from this gene
cDNA EST yk107a2.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGVLVSFNPHLKNQFTFWATGYKAQYDDYLSTLKSMTEKVIKERRAAHDSGEVEKETS
KRMMFLDLMLSMEESNQLTSEDIRQEVDTFMFAGHDTTTSSTSWACWNLAHNPNVQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVYKEMIEVFGDDPNTDITLENVNNLNYLDIVLKESKRIIAPVPALQRKLTNDLEIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA98515.1"
/db_xref="GI:3878483"
/db_xref="SFTREMBI:021424"
/translation="MTIFIPISIAIILAYLATWIPTLLKYKRHWQYGSKLPGPPAHPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="contains similarity to Pfam domain:
(Cytochrome P450), Score=332.4, E-value=1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTEDLKFSMNELVNAEFNSFIQISICCAQIRPTDETARNYLLNGMQFALKHCNEIGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(23517. .23550,23983. .24056,27146. .2
27716. .27902,27954. .28159,28296. .28568)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.2%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST CEMSH91R comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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TITLE
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prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene
                                                                                                                                                                                                                                                                                                                     The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-MAR-2000) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:2335089.
                                                                                                                                                                             Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                       overlaps. For detailed information, please see the TIGR web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence and analysis of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
(http:
                                                                                                                                                                                                                                                     (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin, X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402 (6763), 761-768 (1999)
20083487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1
/www.cbs.dtu.dk/services/NetGene2/), searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 of the plant Arabidopsis
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prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genescan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://gnomic.stanford.edu/GENSCANW.html), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wast.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit; http://genome.washington.edu/RW/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.

We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J5, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

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FEATURES
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                                                                                                                                                                                                                                                                                                                   mRNA
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                                                                                        Complement(join(<432..513,610..671,753..886,979..1282, 1353..1445,1532..1668,1807..1957,2194..2301,2379..2488, 2590..2725,2803..2944,3049..3182,3286..3468,3518..3528,3683..3870,3971..4067,4178..4219,4329..4412,4721..4903,5265..5298,5418..5596,5983..6561,6592..6684,6974..7045,7131..7185,7641..7825,7904..8002,8302..8388,9924..8986,9178..9248,49595..9707,9796..10004,10208..102897,10381..1049,10630..10818,11403..11611,11937..12153,12524..12606,12705...12873,12977...>13035)
                                               complement(<432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .83145
                                                                          /gene="At2g41700"
                                                                                                                                                                                                                                                                                                                                      /note="Sequence from clone T32G6"
                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
"At2g41700"
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CDS
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RFLPFYLMLLEYGLAIASSTYCLTFFFTEHSMAQATSSYSVLLPISLFVFSESSRVIL
MVHFFSGLILMVISFVMGLIPATASANSYLKELLIFFYLQNFFRLSFPGFCFSDGLAS
LALLAQGMKDKSSHGYEBMNYTGASICYLGLEVRLEYCRYSMLLLSFPHGFTRUSLIL
YTIGASRLTELIYDRVYSTSFSTEPLLKDSTGAISTDMEDDIDVQEERDRVISGLSDN
THLYLQNLRXYYPGDKHHGPKVAVQSLTFSVQAGECFGFLGTNGAGKTTTLSMLSGEE
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VRNLHKVYASRRGNCCAVNSLOTTLYENQILSLLGHNGAKKSTISMLVGLLFPFSGD
ALILGNSIITNNDEIRKELGVCPQHDILFPELTTYREHLEMFAVLKGVEEGSLKSTVD
MAEEVGLSDK.INTLVRALSGGMKRKLSLGIALIGNSKVIILDEFTSGMDPYSMRLTWQ
LIKKIKKGRIILLTTHSMDEAEELGDRIGIMANGSLKCCGSSIFLKHHYGVGYTLTLV
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1353..1445,1532..1668,1807..1957,2194..2301,2379..2458,
2590..2725,2803..2944,3049..3182,3286..3468,3518..3622,
3683..3870,3971..4067,4178..4219,4329..4412,4721..4903,
5265..5298.5418..5596,5983..6561,6592..6684,6974..7045,
7131..7185,7641..7825,7904..8002,8302..8388,8924..8986,
9178..9284,9595..9707,9796..11004,10208..10297,
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12524..12606,12705..12873,12977..13035))
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complement(join(17467. 17523,17579. 18237,18321. 1838
18729. 18779,18860. 18933,19114. 19202,19292. 19300,
19447. 19529,19870. 20096))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIRRARSACRDRKTVAFOFIIPAVFLLFGLLFLOLKPHPDQKSITLTTAYFNPLLSGK
GGGGPLPEDLSVPIAKBVAQVIEGGWIDZHRWTSVFPRWFEALADAIDAAGPTLGPT
LLSWSEFLWSSEFDQSVQSRBEGLSSHDSCNPDQSLGYTVLHNGTCQHAGPIYINVML
LLSWSEFLWSSEFDQSVQSRBEGLSSHDSCNPDQSLGYTVLHNGTCQHAGPIYINVML
AAILRLATGNKNMTIQTRNHPLPPTKTQRIQRHDLDAFSAAIIVNIAFSFIPASFAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTSPTVSVAAHIVHRHIPSATCVSEVGNEISFKLPLASLPCFENMFREIESCMKNSDS
DYPGIQSYGISVTTLEEVFLRVAGCNLDIEDKQEDIFVSPDTKSSLVCIGSNQKSSMQ
PKLLASCNDGAGVIITSVAKAFRLIVAAVWTLIGFISIQCCGCSIISRSMFWRHCKAL
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KIDLTGYIKWWGANKNRQPESSSKASEDANVEDAGTELKTLEHTSHATEPYKAPNLGV
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Qvylgayddeeaaaraydlaalkywgpgtlinfpvtdytrdleemonlsreeylaslr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(13464. .13494)
/rpt_family="POLY_A"
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/note="Sequence from clone TllA7"
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DNVVTEKLVEFDLLKHSHKPSFTLSGGNKRKLSVAIAMIGDPPIVILDEPSTGMDPVA
KRFMWDVISRLSTRSGKTAVILTTHSMNEAQALCTRIGIMVGGRLRCIGSPQHLKTRY
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EKNNGKATEKPVVSHGVALGGAAALSLQKSMYPLTSLLTAPLLTNYNTLDPLADPTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(<17467. .>20096)
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IPLPIFAEWWLTKEKFSALDSFIQSSFPGATFKSCNGLSIKYQLPFGEGGLSLADAFG
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RAHYGLRWSNIWRASSGVSFFVCLLMMLLDSILYCALGLYLDKVLPRENGVRYPWNFI
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9. .18779,18860. .18933,19114. .19202,19292. .19300,
7. .19529,19870. .>20096))
                                                                                                                                                                                                                                                            "putative AP2 domain transcription factor' id="AAC02777.1"
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72816 AATGAGAATTTCCACTCGGCAAAGATAGCCATGTGTATTTACAGAAGGCTTCTGGTCACT 72757
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Direct Submission

Direct Submission

Sequencing Facility, DOE Joint Sendmitted (30-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US: On Apr 25, 2001 this sequence version replaced gi:8576174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACO27346 68575 bp DNA HTG 25-APR-20 HOMO sapiens chromosome 16 clone CTD-2519D12, WORKING DRAFT
                                                                                                                               2 (bases 1 to 68575)
DOE Joint Genome Institute
                                                                                                                                                                                                                          Sequencing of Human Chromosome
                                                                                                                                                                                                                                                              DOE Joint Genome Institute
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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TTCLLKGYGRSRQPGKAKEVFLMMRKERKPNVTYNALIDAYGSNGFLAEANGIFRQ
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AELEKAIALYQSMRKKKVKADSVTFTILISGSCRMSKYPEAISYLKEMEDLSIPLTKE
GQVTEAESIFNQMKMAGCEPDVIAYTSMLHAYNASEKMGKACELFLEMEANGIEPDSI
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21547. .21679,21776. .21980,22070. .22175,22312. .23385,
23520. .23625,23720. .23892,23976. .24320))
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MMDPYLPSLSIGLTNQMLHLFGKSGKVEAMMKLFYKIIASGVGINLKTYAILLEHLLA
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1 to 68575)
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/note="T11A7.17; |
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<26681. .>27040
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                                                                                                                                                                                                                                                                                                                                                      Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                      Primates;
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Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                         Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8;
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                                                                                                                                                                                                                                                                                                                            Hominidae;
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Consensus quality: 43126 bases at least Q40
Consensus quality: 46452 bases at least Q30
Consensus quality: 46452 bases at least Q30
Consensus quality: 46452 bases at least Q30
Estimated insert size: 53000; agarose-fp estimation
Estimated insert size: 65075; sum-of-contigs estimation
Quality coverage: 8.56 in Q20 bases; agarose-fp estimation
Quality coverage: 6.98 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 36 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Joint Genome Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: CITB-E1_2519D12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.jgi.doe.gov
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Submitted (14-MAR-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                         Published Only in DataBase (2001) In press 2 (bases 1 to 161818) Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                            Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA,
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Oryza sativa chromosome 1 clone
PROGRESS ***, in ordered pieces.
                                                                Direct Submission
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced
                                                                                                                                                                                                                                                                 On Apr 12, 2001 this sequence version replaced gi:13027286.

Genes were predicted from the integrated results of the following:
GENSCANI.O, BLASTN2.O, BLASTX2.O as well as SplicePredictor
(October 1998 experience sequence was searched against
classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering
                                                                               NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein is
                                                                                                                                                                                                                                                                                                                                                                                    Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaakidabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (cultivar:Nipponbare) DNA, clone:P0460E08 Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAC clone: P0460E08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 161818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c. This
n as it is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from T7 to SP6 of the PAC clone. Detailed information on overlap and assembly quality together with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation of this entry is available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB61195.1"
/db_xref="GI:14597284"
/db_xref="GI:14597284"
/translation="MRADRLMAEGGKRIDLGAPLRSVRHADALPYHKADLNSGPVRHP
/translation="MRADRLMAEGGKRIDLGAPLRSVRHADALPYHKADLNSGPVRHP
GAVPFVWEQRPGQPKSVWTRRAPPSPTTASHPQPLEHGVEDEIDGSPYHDALGEHYVG
ILHGVDASPACSRTGAPAPAPARDEKRAQVAEAAVLQAKKEVTEKQVVSVAAVLRKGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAAQAVAIGSPQYTFRKAGAASATSNSGRELARAAGSNASGSSGDDPGRRTPQSWEDV
YKHKLEQKYVRPGEDGRSKLTSESNQLTFWSDSQAGNGSSPFHHSAGGGLIECRTPVL
GVARPKREFARKFPPSITKREFARKFPPPSLGLDLLLYLKGLPHGPNNLT"
                                                                                 GLHKEYAITINSDGLFHGSQSCVGNLKSNFTGTKFTIRDWQPPYEGAKAFSSRSGRWF
GNKHRCPLVSTGDVEVGEVSYKYSLLRPRGPRRMSCSVQCPVLKGTAVDPQDGKRLSN
SIPSSLVLNSKVPSWHEHLQCWCLNFHGRVMVASVKNFQLIAPVEPGEPSDKTVVLQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MDPEPHRVDASLAPNPSRRQPLLRPGKSTAFKREERRKRKERKQ
QERLALDLERWEPLGAPPRPAAAAASPSRÅALPDKPWVCDPPPEPEPSASWGCGWGPP
AAEPPREPPVPAAVSPQAAAVEACRAFFGEHVDHDDGDDEDEEEEGNVARFFQELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(15923 . 16636, 16711 . .16809)
/gene="p0460E08.3"
join(15923 . .16636, 16711 . .16809)
/gene="p0460E08.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(9680. .10489,10922. .11084,13870.
/gene="P0460E08.2"
join(9680. .10489,10922. .11084,13870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="contains ESTs AU082216(C62661),C28874(C62661)unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7833. .8249)
/gene="p0460E08.1"
                                                     GKIDDDVFTMDYRQPLSAFQAFAICLSNFGTKLA"
                                                                                                                                                                 GAGEERWSALVPDLLADILRCVEAGSERWPPRRDVVACASVCRRWRDVAVAVVQPPLE
SGKITFPSSLKQPGPRDAPMQCFIKRNKKNSTFFLYLGLTQELTDDEKFLLAARRCRR
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/db_xref="G1:14587286"
/translation="MVPWRRSSSSSSAPSSRPARRPARTNARVSPDVSSELSPLAGEE
                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(17683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(17683. .18229,18366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDAGLRGFYEAEREKGRFLCLVCEGIGARAGKRFAGCAALVQHAGSVARAGRRMAHRA
FADAVGRLLGWSAGRTTALQMQTDSDNAGMCDEDIHCEDVPQSAEMEMCPHQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDDDDEERFSDALDTLSRTESFTVNCSVSGLSGMPEPTSRAAAGAEAGVRGIMMDRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Join(9680. .10489,10922. .11084,13870. .14051)
/gene="p0460E08.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRQRRRTRTCATMAARPWTWTLRRMQRRVARVHRLLRAGPRPRAMRTAGRLISRPLAPSPLQLSRKSYMDLLSPIIVRPDNNWFVGCGLIHVCN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0460E08.1"
complement/7000
                                                                                                                                                                                                                                                                                                                                                                                       19584. .19925)]
                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="P0460E08.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19584. .19925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAB61196.1"
/db_xref="GI:14587285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MVAAVAEADEVGGDSCSGQGRRQRHTEATSMVDKDEGSGGRSGQ/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAB61194.1"
/db_xref="GI:14587283"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="P0460E08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4530"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryza sativa"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                           /gene="P0460E08.4"
                                                                                                                                                                                                                                                                                                                                                                                                                 .18229,18366. .18495,19014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .18495,19014.
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CDS
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                                                                                                                                                  RROYDGAKADIWSGGVILFALMAGYLPFHDHNIMVIYRKIYNGEFRCPRWFSKDFTRL
ITRLLDANPKTRITVPBIIESDWFKKGYKPVKFYIDDKSLOVENSCHURDPVPP
PLGLAPPVPPPPQGDDPDGSGSESDSSVVSCPATLSTGESCHVRGSLPRPASLMAFDY
ISFSKGFNLSGLFEERGNEIRFVSGEPMSDIVKKLEEIAKVKSFTVRRKDWRVSIEGT
                                                                                                                                                                                                                                          KYELGRVLGQGSFAKYYQARHLETDECVAIKVLDKEKAVKGGMVHLVKREINVLRRVR
HPNIVQLFEVMASKTKIYFVMEYVRGGELFSRVSKGRLREDTARRYFQQLVSAVDFCH
ARGVFHRDLKPENLLVDENGDLKVSDFGLAAGPDQFDPDGLLHTFCGTPAYVAPEVLR
                                                                                                                                                                                                                                                                                                                                                                                                          complement(36914. .38476)
/gene="P0460E08.9"
/note="contains EST D48640(S14969)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAB61200.1"
/db_xref="GI:14587289"
/translation="MRNNGPAADCRAVRHHKRRGALVARAGRHHCRGRPTMPPTDALT
CSYTSAKAAAAQQVQCEGSL"
CSYTSAKAAAAQQVQCEGSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLSRSPRFPEPVARRYFQQLITAVEFCHSRGVYHRDLKPENLLLDARGDLKVTDFGLS
ALDGGLRGDGLLHTTCGTPAYVAPEVLLKRGYDGAKADIWSCGVILFVLLAGYLPFNE
TNLVILYRNITESNYRCPPWFSVEARKLLARLLDPNPKTRITISKIMDRPWFQQATCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="ospk4-like protein"
/protein_id="BAB61199.1"
/db_xref="051:14587288"
/translation="METTSQDSQVIMGRYKLGRLLGRGTFAKVYKAYKLATGEAVAIK
VFDKEAVQRSGTVEQVKREVDVMRRVHHRHVIKLHEVMATRSKIYFVMEYASGGELFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(28620. .30044)
/gene="P0460E08.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(23452. .24335)
/gene="P0460E08.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GI:14587287"
/translation="MRRAHAGHGSRWNTRTGGADRGRPVPTSAGLAPTWRLRGCHVGWREVDDDAGRMGRRTTGASGGANHGDTGENEHTGWLHETRGDEPTARIRRKLDGGESRRRQDAVGKGENGDEVTRGRFPAVRASTRPRESDASVGLGGATPSEAGDERVLRSSSGRRRQPAVGKGENGDEVTRGRFPAVRASTRPRESDASVGLGGATPSEAGDERVLRSSSG
complement(join(39824.
41406. .41457))
                                      41406. .41457))
/gene="P0460E08.10"
                                                                 complement(join(39824.
41406. .41457))
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="P0460E08.9"
complement/2602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="P0460E08.8"
join(3407-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WAWQGGDSPPLVPAAGRRPITKRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGDMSLVASAPSVLLARKEASQOHDDEEDDGFAREKKKRSNVIMSSPVIDVRPSSMNA
FDIISRSRGLDLSKMFDAEERRSEARFSTRETTTAIVSKLEEIAEAGRFSFKLKEKGR
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/db_xref="GI:14587290"
/translation="MLMATVSPARREPTPQAVRASPMPSAAAALVRRGGGGSGGTVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VELEGSQDGRKGALAIEAEIFKVAPEVHVVEVRKTGGDSPDFRDFYKQELKPSLGDMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(28620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similar to Oryza sativa chromosome 1, P0489A05.16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pseudogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="P0460E08.6"
complement/????
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                                                                                                                                                                                                                                                                                                                                                                         /product="OsPK7"
                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(34076. .34252,34827. .34844)
/gene="P0460E08.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(34076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probably inactive due to stop codon(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGGEHTASDGNGRGGAD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="P0460E08.5"
/note="hww-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains ESTs C22495(E0142),C22494(E0142)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0460E08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="probably inactive due to no initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .d-"BAB61198.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20. .30044)
3.7"
                    .39920,40576. .40677,41062.
                                                                                     .39920,40576. .40677,41062.
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                      .41248,
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ORGANISM
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Best Local
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Best Local :
                                                                 53707 ATTGTATATATAGATCGCTTACTAAACTAATGGCAACAGTTTAATAGAACTAAACTGAT 53766
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66 ctgactggtaagtttcacatgtaaggtgatacttatcttcaaatttatt 113
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962 TACCAGAATGACCCCCTACTGGTGCAGTGTGAAGGTTGGCCAAAATCTTTTGTTGAACCT 903
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                                                                                                                                                                                                                                                                                                                                 Rockville, MD, USA
This sequence was identified as CDM:10210186 by the submitter.
For more information on this record e-mail to fly@celera.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
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HTG; HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. This sequence will be replaced by the finished sequence as soon as it is the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 63904)
                                                      Conservative
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/gene="P0460E08.11"

/note="probably inactive due to frameshift(s) in probably inactive due to stop codons(s) in CDS
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complement(47319. .
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                                                                                                                                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                 1. .63904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAB61202.1"
/db_xref="GI:14587291"
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                                                                       Score 29.6;
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Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connort, T., O'Donnell, P., McGurk, A., McKernan, C.H., O'Connort, T., O'Connell, P., McGurk, A., McGurk, A., McKernan, C.H., O'Connort, T., O'Connell, P., McGurk, A., McGurk, A., McKernan, C.H., O'Connort, T., O'Connell, P., McGurk, A., McGurk, A., McKernan, C.H., O'Connort, T., O'Connell, P., McGurk, A., McG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced gi:6467063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton,
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                                                                                                                                                                                                                                                            overlap relationships among However, it should not be as
                                                                                                                                                                                                                                                                                                                      NOTE: This record contains 82 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                             will be sequenced to completion.
                                                                                                                                                                                                                                                         However,
                                                                                                                                                                                                                                                                                       arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                             the record
                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: L3728 Center clone name: 19_F_12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome
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Eutheria; Primates;
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                                                        o of 100 bp contig of 826 bp in 1 of 100 bp contig of 860 bp in 1
                                                                                                             contig of 10
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                         of 100 bp contig of 870 bp in
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be assumed that this clone
benipletion. In the event that
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27336 28210: contig of 875
28211 28310: gap of 100 l
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16618 17504: contig of 887 bg
17505 17604: gap of 100 bp
17605 18479: contig of 875 bg
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14582: contig of 861 b
1682: gap of 100 bp
15537: contig of 855 b
5637: gap of 100 bp
16517: contig of 870 bp
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38021: contig of 8
3121: gap of 10
39018: contig of 8
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24369: contig of 902 bp
69: gap of 100 bp
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23367: contig of 844
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70336: contig of 876
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66396: contig of 876
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                                            attgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgca 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gelniker, S.E., Georgé, R.A., Galle, R.F., Hoskins, R.A., Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Mentifler, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L. and Kimmel, B. Sequencing of Drosophila chromosome 2L, region 25F3-26A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-JUL-1998) Berkeley Drosophila Genome 64-121, Lawrence Berkeley National Laboratory, One Berkeley, CA 94720, US
Sequence submitted by:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and relationship to other sequences, please visit our seq archive Web site (http://fruitfly.berkeley.edu/sequence/) email to drosophila@mhgc.lbl.gov. Library locations: 45-68, 50-32.
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Berkeley, CA 94720

For further information about this sequence, including its location for further information about this sequence visit our sequence.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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Muscomorpha; Ephydroidea; Drosophilidae; Dro
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Lawrence Berkeley National Laboratory,
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                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                              /clone="PIS DS06477 (D116) and DS03026 (D126)"
/note="DS06477 (d116) extends from bp 1 to bp 84,543
DS03026 (d126) is a bridge extending from bp 83,209 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster
/db_xref="taxon:7227"
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CE 2 (bases 1 to 166441)

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RS Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

RS Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

ROGERS, V., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,

Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,

Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,

Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,

Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,

Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,

McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,

Phouanenavong, S., Pittman, G.S., Patel, S., Pfeiffer, B.,

Phouanenavong, S., Pittman, G.S., Patel, S., Feiffer, B.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,

Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Direct Submission

Berkeley, CA 94720, US

Sequence submitted hy:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,F.G., Brandon,R.C., Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A., Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M., Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibeymam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F., Stapleton,M., Strong,R., Svirrskas,R., Tector,C., Williams,S.M., Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C. Sequencing of Drosophila chromosome 2L, region 25F-26X
                                                                                                                                                                                                                                                                                                                                                                                                               archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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                                /clone="BACR48E14 (D1326)"
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
pBACe3.6)"
                                                                                                                                                                                                                                        /organism="Drosophila
/strain="y; cn bw sp"
/db_xref="taxon:7227"
                                                                                                                                                                           /map="25F-26X"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85264 ATTGTATATATTAGATCGCTTACTAAACTAATGGCAACAGTTTAATAGAACTAAACTGAT 85205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85204 TTATCTCATAAACTTAGCATCTAAATTGATACTTAATTAGCACTTACT 85157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 ctgactggtaagtttcacatgtaaggtgatacttatcttcaatttatt 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 attytaaatytyagatyccttacaaccctyatyacctaatyycycaatycyagyyctyca 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE003611 AE002690
AE003611.2 GI:10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
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                                    20196006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miklos,G.L., Abril,J.F., Agbayani,A., An,H.J.,
Andrews-Pfannkoch,C., Baldwin,D., Ballew,R.M., Basu,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muscomorpha; Ephydroidea; Drosophilidae; Drosophila 1 (bases 1 to 259973)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fruit fly
   (bases 1 to 259973)
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Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 166441;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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AUTHORS

Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.

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COMMENT
FEATURES
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JOURNAL
                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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                                                   CDS
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On Oct 9, 2000 this sequence version replaced gi:7297008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Sul
Submitted
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TKQICYQTLLGVAYCHKQGCLHRDIKPENILLTAQGQVKLCDFGFARMLSPGENYTDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RWSCEKLTKHSYFDDYTAKQRELEHVNSLEAANLRQQQLASQQFMLATAAQQLQTGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLLPRHIQIFGQNEYFKGITLPVPPTLEPLEDKMPAKSQQNPLTIDFLKKCLDKDPTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <16590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="FLYBASE:FBan0007236"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="CG7236"
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'db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product-"CT22313"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .259973
                                                                                                                                                                        ement(<22642. .>24295)
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gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .20287,20339. .>20411))
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CDS

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QVLVVWLNQSPDYAEISRWYTGWKSMLSEPLLREPSVKEHLRRALEIMHRASDTLLQP
                                                                                                                                                                                                                                                                                                                               SSAAAWQPKEHPPMASLLDAWAPLLPSWVLDSVLEQLVLPRLVAGVQEWDPLTDTVPI
DSWVLPWHAILGSKLEEAVYPQIRSKLGIALRAWSPHDRSARAMLTPWQKAFPEEEMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAMEQHTRGIGAKLLLQMGYEPGKGLGKDLQGISHPVQAHVRKGRGAIGAYGPETAAS
IGGKTNKSIKVDEDVREAKEFKDQLNKWRKGSAGGAEPMERQGKRYYYKSVEEVIAKG
HTSGHLLSEKLSKKLGNVRVIDMTGPEKRVLSGYHALGQAKITPEETLYDTEATEKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFDERVTWEGQSNKRIQVSYYCSQVSVSQCNLLLQNYAMCLLDYEYHVLSPAFLVHSP
GIKQSSKADSTRLQYAKEMTKEIKNKIEPEYRVLFGKNSACKT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGQKSVGLLLSNESNPSRFSANFHLANDQHPKIIRREDSARTKELRSLLKCRDRSLRF
ERLQHGEFWLLQNLVMGRKSREVGCAESVTYTTNGDFTFFDNLEMVVSRWRAPVSFAI
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                                                                                                                                                                                                                      TVTPTPPPPVPPAPVIMMDLIHPPAQLEFKELVSQQCADLGIIFAPLPGRREMGKQIY
                                                                                                                                                                                                                                                                                                                                                                                                                                     APACVFAMPELTHNIQLLVSQCEQQIIAIDNQERECSSQQAALESEHRKLEEIVQLER
NHIRTLEESLERVERLIDNPDLSLPQAERLFRELLVDYAAEFHEFGLADLAAGVIAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EESGGEGGTKRRGRAARKPKDYTMPVNFVAGGIQQAGKKKKKALQADDEKGSQKEGAE
ADQGEESDDSAASGRPAFGQNDPGSSNSSSEEERPTLSRKQPSTTFQHRSHIASERNV
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/db_xref="FLYBASE:FBgn0024191"
/protein_id="AAF52282.1"
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/db_xref="FLYBASE:FBgn0024191"
join(25469._.25577,25629...27907,27971...28102)
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AQVFHLKLCPTCHTIPGQEEWLNRTSRADDHLHVFSKALRKWKFRAWEPFYVSDNTEP
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/db_xref="FLYBASE:FBan0011149"
/db_xref="FLYBASE:FBgn0031732"
/protein_id="AAF52281.1"
/db_xref="GI:7297011"
                                                                                                             /gene="CG14006"
                                                                                                                                                                                                                                                                                                                                                                                                           LKRELVQWQPLENPTEPLPLIKKWRGMLQQGDAAEQQPRNVFDPYSSLIWAGVMPSFR
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                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-primer ET; 73% of reads Chemistry: Dye-terminator Big Dye; 27% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 151162 bases at least Q40 Consensus quality: 152443 bases at least Q30 Consensus quality: 152443 bases at least Q30 Consensus quality: 153249 bases at least Q20 Consensus quality: 153249 bases at least Q20
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Submitted (14-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 10, 2000 this sequence version replaced gi:7021826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 155172)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                Quality coverage: 4.08 in Q20 bases; agarose-fp Quality coverage: 4.69 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                 Insert size: 177000; agarose-fp
Insert size: 154672; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; 73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: H_NH0238P13
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                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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Db 83677 AGGTGCTTTATGCACTTCATTAGCTTATAGAAAAATTGAAATGCTGCAATAATTGTAAAT 8373
On Jan 13, 2001 this sequence version replaced gi:11878000. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tttcacatgtaaggtgatacttatcttcaattttattccacaca 120
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                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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105845. .155172
/note="assembly_name:Contig6"
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/db_xref="taxon:9606"
/chromosome="18"
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/note="assembly_name:Contig3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105744: contig of 43394 bp in 105844: gap of unknown length 155172: contig of 49328 bp in
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Pred. No. 19
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TREMBL;

Wp:, WORMPEP;

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JOURNAL
REFERENCE
AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                   HTG;
                                        Submitted (14-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp,
                                                                                                                              Hattori,M., Ishii,K., Toyoda,A., Fujiyama,A., Yada,T., Totoki,Y., Direct Submission
                                                                                                                                                                                           Published Only in DataBase (2000) In press 2 (bases 1 to 174815)
                                                                                                                                                                                                                                      Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. Homo sapiens 174,815 genomic DNA of 18q23
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923
Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 18
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RP11-70L8 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/HGP/Chr9
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                                                                                                                                                                                                                                                                                                     nmalia; Eutheria; Pr
(bases 1 to 174815)
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sapiens DNA, clone:RP11-635B11.
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by restriction digest data"
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/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP11-70L8"
/clone_lib="RPCI-11.1"
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| Clone RP11-635B11 map 18q23, WORKING
                                                                                                                                                  Taylor, T.D., Watanabe, H.
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COMMENT
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* NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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166715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of
Assembly program: Phrap; version 0.990329
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Center clone name: RP
                                                               114348 114447: gap of
114448 122080: contig
                                                                                                     104598 104697: gap of 104698 114347: cont
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171628
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Contact: hattori@gsc.
 128466
128566
                                                                                                                                                                 73244 73343: gap of 100 bp
73344 83572: contig of 10229 bp in length
83573 83672: gap of 100 bp
83673 94547: contig of 10875 bp in length
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                                                 122180: gap of
 128565: gap of 
135791: cont
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151734 contig of
15576 contig of
159193 contig of
161359 contig of
163515 contig of
166614 contig of
166614 contig of
171527 contig of
173248 contig of
                              128465: contig of 6285
                                                                                                                            547: gap of 100 bp
104597: contig of 9950 k
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Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,
Severy,D., Sougnez,C., Spencer,B., Stange-Thomann,N.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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IN PROGRESS ***, 2 ordered pieces.
                                                                                                                                                                                                                                                                                                              On Jul 26, 2001 this sequence version replaced gi:14994291. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996–1997)
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                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-MAY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RM/RepeatMasker.html
NOTE: This is a 'working draft' sequence. It curconsists of 2 contigs. Gaps between the contigs
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                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
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nes 57; Conserv
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                                                                                               Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid: L00752; 100% of reads Chemistry: Dye-terminator Big Dye. 100% of reads Consensus quality: 195355 bases at least Q40 Consensus quality: 195464 bases at least Q30 Consensus quality: 195468 bases at least Q30 Consensus quality: 195483 bases at least Q20
Insert size: 195491; sum-of-contigs
Insert size: 183499; 21.0% error; agarose-fp
Quality coverage: 10.77x in Q20 bases; sum-of-contigs Quality
coverage: 11.71x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                Center project name: bA149I2
                                                                                                                                                                                                                                                                                                                                                                                                                   requests: clonerequest@sanger.ac.uk
On Jul 17, 2001 this sequence version replaced gi:14596366
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-JUL-2001) Sanger Centre, Hinxton, Cambridgesh CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL449423.11 GI:14787534
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                        Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                    Web site:
                                                                                                                                                                                                                                                                                                                                                                            Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Babbage, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 168134: contig of 168134 bp in length
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168235 178056: contig of 9822
Location/Qualifiers
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/clone_lib="RPCI-11 Human Male BAC"
/30884 c 34094 g 63393 t 100
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/db_xref="taxon:9606"
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Pred. No. 20;
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9 clone RP11-14912, *** SEQUENCING IN
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2 bp in
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Best Local
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AL136230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57;
                                                                                                                                                        The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw., SWISSPROF; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                   This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                       together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission rorresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jul 14, 2000 this sequence version replaced gi:8574123. During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations
                                                Group. Further information can be found at
                                                                            chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                       annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                    only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 120515)
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http://www.sanger.ac.uk/HGP/Chr6
RP1-95I21 is from the library RP
                                                                                                                                                                                                                                                                  feature key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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This sequence will be replaced
by the finished sequence as soon as it is available
the accession number will be preserved.
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1. .195491
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/db_xref="taxon:9606"
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Pred. No. 20;
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library RPCI-1 constructed at the Roswell

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IMPORFANT: This sequence is not the entire insert of clone IMPORFANT: This sequence is not the entire insert of clone RP1-95121 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP1-95121 is at 120515 in this sequence. The true left end of clone RP3-437121 is at 4877 in sequence. The true right end of clone RP1-242N11 is at 100 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
/note="MIR repeat: matches 33.
                                                                                                                                                                   /note="16 copies 2 mer ac 87% conserved"
complement(10277. .10730)
                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="31 copies 2 mer at 71% conserved"
complement(640 . .1130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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                                     note="AluJo repeat: matches 1. .298
                                                                                                                note="match:
                                                                                                                                                                                                                                                                                                                                                                'note="MIR repeat: matches 5. .180 of consensus"
6362. .6475
                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="match: GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="25 copies 2 mer aa 72% conserved" complement(5063...5482)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            932. .4089
'note="LlMEc repeat: matches 890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="match: GSS: Em:AQ595695"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            751. .3929
'note="Alusg/x repeat: matches 134. .310 of consensus"
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                                                                            note="match:
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                                                                                                                                                                                                                                                                :e="MER5B repeat: matches 1. .173 of consensus"
                                                                                                                                                     e≃"match:
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6. .6934
                                                                                                                                                                                                                                                                                                                                                                                                                e="match: GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lement(5957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ="L2 repeat: matches 2575.
.5951
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                                                                                                                                                                                                             .7640
                                                                                                                                                                                                                                              .7428
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                                                                                                                                                                                                                          repeat: matches 2575. .2702 of
                                                                                                              GSS:
                                                                                                                                                 GSS:
                                                                      GSS: Em:AQ082251*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .6576)
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                                                                                                                                                   Em: AQ839431"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Em: AQ630441"
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                                                                                                              Em: AQ716569'
 .232 of consensus"
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                                                                                                                                                                                                                                                                                                                                           .161 of
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                                     of consensus"
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/note="LIPAR11 repeat: matches 5694. .6165 of consensus"
33041. .33473
/note="MLT2FB repeat: matches 1. .414 of consensus"
complement(34176. .34667)
                                                                                                                                                                                                                    38624. .38694
/note="AluJ/FRAM repeat: matches
                                                                                                                                                                                                                                                                              36513. .38620
/note="MER57-internal repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(12939. .13175)
/note="match: GSS: Em:B85743"
                                                                   consensus"
                                                                                      /note="MER57-internal
                                                                                                                                             /note="MER57-internal repeat:
                                                                                                                                                                                                                                                              consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         35336. .35696
                                 'note="MER57B
                                                                                                                                                                                     'note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                     note="MER57B repeat: matches 1. .399 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"HAL1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MER5A repeat: matches 9. .182 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="match: GSS: Em:AQ835474"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 1170. .1526 of consensus"
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repeat: matches 2010. .3753 of consensus*
                                   repeat: matches
                                                                                                                                                                                                                                                                                                                                                          repeat:
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                                                                                          repeat:
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                                   1. .403 of consensus"
                                                                                            matches
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RESULT 35
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                                                                                                                                                                                                                                                                                 Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Maddonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tttcacatgtaaggtgatacttatcttcaa 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 20, 2000 this sequence version replaced gi:9123835 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52; Conserver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C. and Lander, E Homo sapiens, clone RP11-11123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 159073)
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Homo sapiens clone RP11-11123,
                                                                                                                                                                                                                                           Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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Contact: sequence_submissions@genome.wi.mit.edu
                      Web site: http://www-seq.wi.mit.edu
                                             Center code: WIBR
                                                                   Center: Whitehead Institute/ MIT Center for Genome
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/note="match: GSS: Em:AQ89442)
complement(50343. .50444)
/note="match: STS: Em:L17929"
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/note="L1PA15 repeat: matches 5499.
49295. .49393
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/note="LlPA15 repeat: matches 3753.
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                                                                                               -- Genome Center
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nusbaum, C., Lander, E., Allen, N.,
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SS: Em:AQ894428"
3. .50444)
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Homo sapiens chromosome SEQUENCE, 5 unordered pi

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4 clone RP11-352I24 map 4, WORKING DRAFT

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RESULT 3
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Best Local S
Matches 61
                                                                                       4146
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                                                                                                                                                                                                              10 taaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcactga 69
                                                                                       CTGGTATCTATTACTTGAAAATTTATAATAGACTTCAACCTAGTCCACATGAAA 4093
                                                                                                         ctggtaagtttcacatgtaaggtgatacttatcttcaattttattccacacaaca 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently * consists of 5 contigs: The true order of the pleces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 156407 bases at least 040 Consensus quality: 158013 bases at least 030 Consensus quality: 158013 bases at least 020 Insert size: 157000; agarose-fp Insert size: 158073; sum-of-contigs Quality coverage: 5.6 in 020 bases; agarose-fp Quality coverage: 5.6 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                         52902
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Center clone name: 11_I_23
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134634 159073: contig of 24440 bp in length
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27848 c 26048 g
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82143. .108087
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/clone="RP11-11123"
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108188. .134533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_fragment"
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134533: contig of 26346 bp in
34633: gap of 100 bp
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82042: contig of 51354 bp in length
2142: gap of 100 bp
108087: contig of 25945 bp in length
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VERSION
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----- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                              Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehozaky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Naylor, J., Naylor, J., Pierre, N., Pisani, C., Pollara, V., Raymod, C., Riley, R., Rothman, D., Poly B., Connor, B., Connor, B., Connor, B., Connor, R., Pollara, V., Raymod, C., Riley, R., Rothman, D., Pollara, C., Pollara, V., Raymod, C., Rothman, D., Pollara, V., Raymod, C., Rothman, D., Pollara, V., Raymod, C., Rothman, D., Pollara, V., Raymod, C., Pollara, V., Raymod, C., Rothman, D., Pollara, V., Raymod, C., Rothman, C., Pollara, V., Raymod
                             Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
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/clone_lib="RPCI-11 Human Male BAC"
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Vassiliev, H., Viel, R.,
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Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aum, C. and Lander, E. clone RP11-753L19
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FEATURES
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Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 23, 2000 this sequence version replaced gi:8814977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 161482 bases at least Q40
Consensus quality: 165432 bases at least Q30
Consensus quality: 167439 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 169122; sum-of-contigs
Ouality coverage: 4.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L5673
Center clone name: 753_L_19
----- Summary Statistics
Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           142087 142186: gap of 142187 170022: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108750 108849: gap of
108850 142086: cont
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87191 10874
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52353 66785: contig of 14433 bp in length
66786 66885: gap of 100 bp
66886 87090: contig of 20205 bp in length
87091 87190: gap of 100 bp
87191 108749: contig of 21559 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12622 12721: gap of 100 bp
12722 23152: contig of 10431 bp in length
23153 23252: gap of 100 bp
23253 37025: contig of 13773 bp in length
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                                                                                                                                                                                                                                                                 /clone="RP11-753L19"
/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                    7 170022: contig of Location/Qualifiers
                                                                                                                 note="assembly_fragment"
                                                                                                                                                              note="assembly_fragment"
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                    note="assembly_fragment"
                                                                 'note="assembly_fragment"
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3947: gap of 100 bp
12621: contig of 8674 bp in length
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AC068203/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                               Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Van Millon, B. W., V., Warstliff, R., Wall, R., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGTATCTATTACTTGAAAATTTATAATAGACTTCAACCTAGTCCACATGAAA 30241
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Submitted (30-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 25, 2000 this sequence version replaced gi:7671263. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Alleu, Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Deare, K., Diaz, J.S., Cade, D., Collymore, A., Cooke, P., DeArellano, K., Deare, K., Diaz, J.S., Cade, D., Collymore, A., Cooke, P., DeArellano, K., Deare, K., Deare, K., Deare, K., Deare, R., Collymore, A., Cooke, P., DeArellano, K., Deare, K., Deare, K., Deare, K., Deare, Collymore, A., Cooke, P., DeArellano, K., Deare, K., Deare, K., Deare, Collymore, A., Cooke, P., Dearellano, K., Dearellano, K.
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                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                              Vassiliev, H., Viel, R.,
                                                                                                                                                                                                                                                                           Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                   Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will.
                                                                                                                                                                                                                                                                                                               31131 31230: gap of 100 bp 31331 31230: gap of 100 bp 31331 38604: contig of 7374 bp in length 38605 38704: gap of 100 bp 4558: gap of 100 bp 52092 52191: gap of 100 bp 52192 58656: contig of 6533 bp in length 52092 52191: gap of 100 bp 58757 68155: contig of 6465 bp in length 58757 68155: contig of 6465 bp in length 68156 68255: gap of 100 bp 68255: gap of 100 bp 100 bp
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Insert size: 179427; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
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Consensus quality: 172044 bases at least Q40 Consensus quality: 176527 bases at least Q30 Consensus quality: 178383 bases at least Q20
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Center: Whitehead Institute/ MIT Center for Genome
Center code: WIBR
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                                                                                                                                                                                                                                                             Homo sapiens chromosome 4 clone SEQUENCE, 23 unordered pieces. ACQ23187
1 (bases 1 to 181542)
Birren, B., Linton, L., Nusbaum, C.
Homo sapiens chromosome 4, clone
Unpublished
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55; Conser
                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                  AC023187.2 GI:7139717
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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139035. .181127
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DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marguls,N., McEwan,P., McGurk,A., McKernan,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L., NusDaum, C., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Boukett, G., Castle, J., Bouketa, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, J., Bouketa, C., Boukhgalter, B., Collins, S., Collymore, A., Cooke, P., Collins, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Research, 320 Charles Street, Cambridge, MA 02141, USA
on Mar 1, 2000 this sequence version replaced gi:69577
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (09-FEB-2000) Whitehead Institute/MIT Center for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stojanovic, N., Subramanian, A., Talamas, J., Tesfay Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Limmer, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved.
                                                                                                                                                                                                                      3561 3660: gap of 100 bp

3661 5983: contig of 2323 bp in length

5984 6083: gap of 100 bp

6084 8818: contig of 2735 bp in length

8819 8918: gap of 100 bp

8919 11436: contig of 2518 bp in length

11437 11536: gap of 100 bp

11537 14541: contig of 3005 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 166930 bases at least Q40 Consensus quality: 173654 bases at least Q30 Consensus quality: 176417 bases at least Q20 Insert size: 182000; agarose fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 3.9 in Q20 bases; agarose-fp Quality coverage: 3.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: 102_H_15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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                    25666 25765: gap of 
25766 30336: con
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1097 1196: gap of 100 bp
1197 3560: contig of 2364 bp in length
3561 3660: gap of 100 bp
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                                                                                                        22236:
30436:
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18297: contig of 3656 bp
8397: gap of 100 bp
22136: contig of 3739 bp
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                                                                  36: gap of 100 bp 25665: contig of 3429
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Nu,X., Wyman,D.,
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27647 14483
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34702 34801: gap of
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74407 85102: contig of 10696 bp in length
85103 85202: gap of 100 bp
85203 95862: contig of 10660 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55752 55851:
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                                                                                                                                                                                                                                       /note="assembly_fragment" 55852. .65044
                                                                                                                                                                                                                                                                                                                                                                                                             clone_end:T7
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14642. .18297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
11537, .14541
                                                                                            vector_side:left"
                                                                                                                            clone_end:SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34802
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25766. .30336
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/db_xref="taxon:9606"
                                           note="assembly_fragment"
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/clone_lib="RPCI-11 Human Male
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127546: contig of 15560 bp in length
77646: gap of 100 bp
144833: contig of 17187 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 pp
111886: contig of 15924 bp in
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V.aphylla mRNA 1
X91634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphoenolpyruvate carboxylase; ppc gene.
Vanilla aphylla.
Vanilla aphylla
Vanilla aphylla
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Vanilloid clade; Vanillinae; Vanilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-SEP-1995) H.H. Gehrig, TH-Darmstadt, Botanik FB10, Schnittspahnstr. 10, 64287 Darmstadt, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gehrig, H.H.
Direct Submission
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               ELVKLNPTSEYAPGLEDTLILTMKGIAA"
254 c 283 q 266 t
                                                                                      /translation="SDSGKDAGRLSAAWPYYKTQEELVQVAKQFGVKLTMFHGRGGTV
GRGGGGFYHLGILSQPDJTILGSLRVTVQGEVIBQCFGEERLCFRTLQRFTVATLEHGM
HHHISPKPEWRSLMDEMAVLAYKEYRSIVFQBERFVZYFELATPELEYGRANIIKSPB
KRKPSGGIESLRAIPWIFAWTHTRFHLPVWLGFGAAFKHVITKDIRNLHILREMYNGW
                                                    PFFRVTIDLIEMVFTKGNPGIASLYDELLVSNDLLSFGMELRANYEETKRLLLQVAGH
KDLLEGDPHLKQRLRPRDPYITTLNVCQAYTLKAIRDQVTTQWRTHVSNETESRKSAA
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111987. .127546
                                                                                                                                                                 /db_xref="SPTREMBL:004918"
                                                                                                                                                                                 /product="phosphoenolpyruvate carboxylase"
/protein_id="CAA62828.1"
/db_xref="GI:2145479"
                                                                                                                                                                                                                                                          /gene="ppc"
/EC_number="4.1.1.31"
                                                                                                                                                                                                                                                                                                                /gene="ppc"
                                                                                                                                                                                                                                                                                                                                                   'tissue_type="shoot"
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31041 c 31307 g 56823 t
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163055. .181542
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144934. .162954
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127647. .144833
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burgdorferi group.

1 (bases 1 to 17078)

1 (bases 1, Casjens, S., Huang, W.M., Sutton, G.G., Clayton, R., Fraser, C.M., Casjens, S., Huang, W.M., Dodson, R., Hickey, E.K., Lathigra, R., White, O., Ketchum, K.A., Dodson, R., Richardson, D., Gwinn, M., Dougherty, B., Tomb, J.F., Fleischmann, R.D., Richardson, D.,
                                                                                                                                                              Borrelia
AE001152
                                                                                                                                                                                                                                                                                                                                                                                         51;
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                                                                                                     Borrelia burgdorferi
                                                                                                                                                  AE001152.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-DEC-1999) Celera Genomics, 45 West Rockville, MD, USA
This sequence was identified as CDM:10213067 by
For more information on this record e-mail to fl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 14039)
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                                                                                   Bacteria; Spirochaetales;
                                                                                                                   Lyme disease spirochete.
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/db_xref="taxon:7227"
3093 c 3021 g 3932 t
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melanogaster,
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Pred. No. 28;
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                                                                                     Spirochaetaceae;
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                                                                                       Borrelia
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gene	gene CDS	gene CDS		gene CDS	TITLE JOURNAL FEATURES	TITLE JOURNAL MEDLINE REFERENCE AUTHORS
/note="hypothetical protein; identified by Glimmer; /note="hypothetical protein; identified by Glimmer; putative" /codon_start=1 /codon_start=1 /transl_table=11 /transl_table=11 /product="B. burgdorferi predicted coding region BB0475" /protein_id="hARC66868.1" /protein_id="hARC66868.1" /db_xref="GI:2688417" /translation="hMKAQKEKLKLIPILVISGILIVFMSCMKTSTIKSKENAKEITY /translation="hMKAQKEKLKLIPILVISGILIVFMSCMKTSTIKSKENAKEITY / LISTIKINQKVEIVNYKSDSKNNLIITLKNKSTEDINANSLAIFKEGSKTGELIREKL NGLEFKTFHLKTKINTKRKTTLYIFEKQ" 27853990 /gene="hBB0476"	/product="B. burgdorferi predicted coding region BB0474" /protein_id="AAC66869.1" /db_xref="GI:2688418" /translation="MAYLFLINLMFLALKIDFRFFVNLFLSVIVCLQ" complement(19232315) /gene="BB0475" complement(19232315)	IVERINALINIPVYFIFQYFGIMENSLGYAFIISNYLAIIILIAFTCTRYWYKPILI KKYK" 17641865 /gene="BB0474" 17641865 /gene="BB0474" /note="hypothetical protein; identified by Glimmer; putative" /codon_start=1 /transl table=11	/product="conserved hypothetical integral membrane /product="conserved hypothetical integral membrane protein" /prodein_"d="AAC66867.1" /db_xref="G1:2888416" /db_xref="G1:2888416" /translation="MSTDKSKTRELILINGNLYKVLFLISFPIVITNIIQAFYDLTDMF /translation="MSTDKSKTRELILINGNLYKVLFLISFPIVITNIQAFYDLTDMF YVGKLGAMPLSALSLAGDVNFFIIAIAMGMATGSISLMSKCIGEGNFSRESRYAGQLI VLNFYLSLEYVTICAFFIIDHLDLGVKGELKELSRYVFYVTIFAF PMFLSISTYI VLNAGGETILSWTIVLFANIVWFILDFILIESFNGTTGAAWATLFSKLLTVVFYLFLT YRLNYGLKIHLKDLVIDIRSIKEIVNLGAKKVNRVEEVLKKGFFFISLAILIIN AYGLTNTISFTLFLAMGIGTGIISIVGQNLGAKKVNRVEEVLKKGFFFISLAILIIN SIVLFNKGFTILRLTNNDLEYLNYANYLLTTIGTRGYGLGVFFGGLIGSGRTKIAM TVITTERUTTTICATURENTERVENTER	/organism="Borrelia burgdorferi" /db_xref="taxon:139" 361 .1725 /gene="BB0473" 361 .1725 /gene="BB0473" /note="similar to SP:P54181 PID:1256651 GB:AL009126 percent identity: 23.93; identified by sequence similarity; putative" /codon_start=1	Rachardson, D., Peterson, J., Kerlavage, A.K., Quackenbush, J., Salzberg, S., Hanson, M., van-Vugt, R., Palmer, N., Adams, M.D., Gocayne, J.D., Weidman, J., Utterback, T., Watthey, L., McDonald, L., Artiach, P., Bowman, C., Garland, S., Fujil, C., Cotton, M.D., Horst, K., Roberts, K., Hatch, B., Smith, H.O. and Venter, J.C. Direct Submission B., Smith, H.O. and Venter, J.C. Submitted (12-DEC-1997) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location, Qualifiers	Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van Vugt,R., Palmer,N., Adams,M.D., Gocayne,J., Venter,J.C. et,al. Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi Nature 390 (6660), 580-586 (1997) 98065943 2 (bases 1 to 17078) 2 (bases 1 to 17078) Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A., Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B., Tomb,JF., Fleischmann,R.D.,
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RESULT 43
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fruit fly.

Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eteryota; Meotazoa; Arthropoda; Diptera; Brachycera;

Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 49759)

Adams, M.D., Celniker S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,

Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F.,

George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N.,

Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X.,
                                                                                                                                                                                                                                                                                                                                         sequence.
AE002717
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5986. .6819
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identified by sequence similarity; putative"
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GGYAMILASDGNYVTVKLSSGEMRLIFKKCIATIGEIGNEDYANISIGKAGKSRWLGR
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GaaikELFnVTPvSCNLLniksKaKvvvsrKGYpiGKGKTSSmKKayvyLKKEDKiDi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dentified by sequence similarity; putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="similar to GP:1685374 percent identity: 98.92;
                                                                                                                                                                                                                                                                                                                                                                                        melanogaster
                                                                                                                                                                                                                                                                                                                     GI:7289774
                                                                                                                                                                                                                                                                                                                                                                                                                49759 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28.8;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                        genomic scaffold 142000013385965, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ť
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GP:1685375 percent identity: 97.83;
uence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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REFERENCE
AUTHORS
TITLE
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Wei,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z.,
Kennison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C.,
Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A.,
Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C.,
McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C.,
Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L.,
Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K.,
Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K.,
Muzny,D.M., Nelson,D.L., Nelson,M., Pittman,G.S., Pan,S.,
Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K.,
Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I.,
Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C.,
Stapleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,R.,
Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A.,
Weinstock,G.M., Weissenbach,J., Williams,S.M., Woodaye,T.,
Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F.,
Zhong,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
NE 20196006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M., Podson,K., Doup,L.E., Downes,M., Dugan-Rocha,S., Dunkov,B.C., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C., Ferriera,S., Fleischmann,W., Fosler,C., Gabriellan,A.E., Garg,N.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Benos,P.V., Berman,B.P., Bhandari,D., Bolshakov,S., Borkova,D., Botchan,M.R., Bouck,J., Brokstein,P., Brottier,P., Burtis,K.C., Busam,D.A., Butler,H., Cadieu,E., Center,A., Chandra,I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brandon,R.C., Rogers,Y.H., Blazej,R.G., Champe,M., Pfeiffer, Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baxendale,J., Bayraktaroglu,L., Beasley,E.M., Beeson,K.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andrews-Pfannkoch,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miklos, G.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 49759)
                                                                                                                                           /db_xref="FLYBASE:FBgn0032948"
/evidence=not_experimental
/protein_id="AAF45446.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <8107
                             LFELVHEKYMVVRGFLSRDKRNLLAGQPATRP"
                                                       AISNYKKTPSERKTLVFIAKKWLHIQMLWREFRLRDKQIRRLGHKDARVLEHGYFQQE
                                                                                    /db_xref="GI:7289775"
/translation="MPNIVALKLSASYPLMPGHKDEGNILALDQLALQQQISANFIFH
                                                                                                                                                                                                                                          /codon_start=1
/db_xref="FLYBASE:FBan0017570"
                                                                                                                                                                                                                                                                                                                                                                         8107.
                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="FLYBASE:FBan0017570"
/db_xref="FLYBASE:FBgn0032948"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="39E1-39E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <8107. .>8511
/gene="CG17570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/chromosome="2L"
                                                                                                                                                                                                                                                                                                           /note="CG17570
                                                                                                                                                                                                                                                                                                                                  /gene="CG17570"
                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="CG17570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
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/db_xref="FLYBASE:FBgn0032948"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="CT34146"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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16286
                                                                                                                                                                                                                                                                                                    gene product"
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BASE COUNT
ORIGIN
                                                                                                                            REFERENCE
AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Locus
                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                         Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Punch, E., Sequeira, A., Sethi, H., Snir, Svirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Rubin, G.M.
                                        Celniker,S.E., George,R.A., Galle,R., Svirskas,R.R., Hoskins,R.A., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Chavez,C., Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster, chromosome 2L, region 38A7-38C9, Pl clon DS04178, complete sequence. AC004735 AC004719 AC000718 AC000719 AC000720 AC000721 L81497 AC0001816 L81498 AC000722 AC000723 AC001208 L81499 L81496 AC000724 AC000725 AC000725 AC000727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila 1 (bases 1 to 74534)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC004735.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fruit fly.
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FKYHEGYNSKLMINDVALIKLSSPVRQTSKIRAIELADSSAVSGTNAVVSGWGTTCFL
FCSSPDTLQKVEVDLLHYKDCAADTYNYGSDSILETMVCATGEKKDACQGDSGGPLVA
DNKLVGVVSWGSCCAWTGYPGVYADVASLRSWIVDTTDSL*
10540 c 10241 g 14491 t
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/db_xref="Gi:7289716"
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/db_xref="FLYBASE:FBgn0032947"
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Mak,J., Mazda,P., Mok,M.S., Moshrefi,A.R., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B.
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Pred.
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Pfeiffer, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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  Punch, E.,
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SOURCE
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                                                                                                                                                                                                   requests: clonerequest@sanger.ac.uk

On Oct 1, 2000 this sequence version replaced gi:9931221.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
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Berkeley, CA 94720

For further information about this sequence, including its location for further information about this sequence, including its location for further sequence, please visit our sequence contains a contain the sequence of the sequenc
annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                         This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human DNA sequence
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Zieran,L.L. and Kimmel,B.E.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (30-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berkeley Drosophila Genome
Lawrence Berkeley National
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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/clone="P1 DS04178 (D78)"
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/clone_lib="P1 library, partial Sau3A in pAd10sacBII"
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/strain="y2; cn bw sp"
/db_xref="taxon:7227"
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ational Laboratory, MS 64-121
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone RP3-472A9 on chromosome 6q13-14.3,
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Search completed: March 19, 2002, 10:00:06 Job time: 1710 sec
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Best Local S
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                                                                                                                                                                                                                                                                                                                      Local Similarity 53.0 nes 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: RMBL; Sw:, SWISSPROT; Tr:, TRRBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6

RP3-472A9 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2

IMPORTANT: This sequence is not the entire insert of clone RP3-472A9 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP3-472A9 is at 85195 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24927 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RP3-472A9"
/clone_lib="RPCI-3"
14629 c 16180 g 29459 t
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53.6%; Pred. No. 30;
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                           O
      92:
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Human secret	AAC59911		452	0		
Parali	AAQ80534		2148			
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	AAX0441		2284	0	25	
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Callithrix jacchus	AAH83942		649	0	5	
Haemophilus influe	AAA92497		3300	0	ŗ	
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## ALIGNMENTS

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10-AUG-1999; 99US-0148171 11-AUG-1999; 99US-0148171 11-AUG-1999; 99US-0148171 11-AUG-1999; 99US-0148181 11-AUG-1999; 99US-0149181 11-AUG-1999; 99US-0149181 11-AUG-1999; 99US-0149181 11-AUG-1999; 99US-0149182 20-AUG-1999; 99US-014923 20-AUG-1999; 99US-0149230 23-AUG-1999; 99US-0150066 27-AUG-1999; 99US-0151066 27-AUG-1999; 99US-0151066 27-AUG-1999; 99US-0151066 27-AUG-1999; 99US-0151066 27-AUG-1999; 99US-0151060 27-AUG-1999; 99US-0151130 31-AUG-1999; 99US-0151130 31-AUG-1999; 99US-0151130 31-AUG-1999; 99US-0151230 31-AUG-1999; 99US-0	PR 26-JUL-1999; 99US-01 PR 27-JUL-1999; 99US-01 PR 27-JUL-1999; 99US-01 PR 27-JUL-1999; 99US-01 PR 28-JUL-1999; 99US-01 PR 02-AUG-1999; 99US-01 PR 02-AUG-1999; 99US-01 PR 03-AUG-1999; 99US-01 PR 04-AUG-1999; 99US-01 PR 05-AUG-1999; 99US-01 PR 05-AUG-1999; 99US-01 PR 06-AUG-1999; 99US-01

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24-MAY-1999

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58; Conservative
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RESULT
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XX BP1C
XX EP1C
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Best Local Similarity 78.9%;
Matches 56; Conservative
  25-FEB-1999
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25-MAR-1999
25-MAR-1999
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01-APR-1999
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16-APR-1999
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24-MAY-1999
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28-OCT-1999;
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termination sequence; ss.
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                             The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors \mathbf{f}_i the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
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                                                                                                                                                                                                             Sequence
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                                                   aggtactacaaatgtgaaatgccgtataactcagatgaactgatggtgcaat 83941
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41; Conservative
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99US-0154603.
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Indels

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Length 1082138;

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0 other;

for

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AAX20248/c

ID AAX20248;

XX AAX20248;

XX D4-MAY-1999 (first entry)

XX Borrelia burgdorferi polynucleoti.

XX Borrelia burgdorferi; spirochete; epidemic relapsing fever; endemic KW epidemic relapsing fever; endemic XX Borrelia burgdorferi.

XX Borrelia burgdorferi.

XX W09858943-Al.

XX (HUMA-) HUMAN GENOME SCI INC.

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   RESULT 11
AAC49264
ID AAC492
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AC AAC492
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Best Local
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                                                                                                                                                                                                                     406588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
      18-OCT-2000
                                      AAC49264;
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                                                                     AAC49264
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                                                                                                                                                   AAATAATCTTATTTTTGACAGAAATGGTTATAAGTATCATGGACTTATTGCA
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                                                                                                                                                                                                                                                                                    1 Similarity
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      (first
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     entry)
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27-MAY-1999;
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07-MAY-1999;
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99US-0132484.
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       Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                 Arabidopsis
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l Similarity 76.1%;
35; Conservative
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                                                  thaliana
                                                                      (first
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990S-0151133

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30-AUG- 31-AUG- 01-SEP- 07-SEP-	27-AUG- 27-AUG-	25-AUG- 26-AUG- 27-AUG-	23-AUG- 23-AUG-	20-AUG- 20-AUG-	18-AUG- 20-AUG-	16-AUG- 17-AUG-	13-AUG-	12-AUG-	10-AUG- 11-AUG-	09-AUG-	06-AUG-		05-AUG-	04 - AUG -	02-AUG-	02-AUG-	27-JUL- 28-JUL-				22-JUL- 22-JUL-	22-JUL- 22-JUL-	21-JUL- 21-JUL-						19-JUL-	16-JUL-	14-JUL- 15-JUL-	12-JUL- 13-JUL-	-TOT-60		
30-AUG-199 31-AUG-199 01-SEP-199 07-SEP-199	27-AUG-199 27-AUG-199	25-AUG-199 26-AUG-199 27-AUG-199	23-AUG-199	20-AUG-199 20-AUG-199	18-AUG-199	16-AUG-199	13-AUG-199	12-AUG-199	10-AUG-199	09-AUG-199	06-AUG-199	05-AUG-199	05-AUG-199	04-AUG-199	02-AUG-199	02-AUG-199	27-JUL-199	27-JUL-199 27-JUL-199	23-JUL-19	23-JUL-19	22-JUL-19	22-JUL-199 22-JUL-199	21-JUL-199 21-JUL-199	20-JUL-199	20-JUL-199	19-JUL-19	19-JUL-19	19-JUL-19	19-JUL-19	16-JUL-19	14-JUL-19 15-JUL-19	12-JUL-19 13-JUL-19	09-JUL-19	06-JUL-19	01-JUL-19
30-AUG-1999; 31-AUG-1999; 01-SEP-1999; 07-SEP-1999;	27-AUG-1999; 27-AUG-1999; 27-AUG-1999;	25-AUG-1999; 26-AUG-1999; 27-AUG-1999	23-AUG-1999; 23-AUG-1999;	20-AUG-1999; 20-AUG-1999;	18-AUG-1999; 20-AUG-1999;	16-AUG-1999; 17-AUG-1999;	13-AUG-1999;	12-AUG-1999;	10-AUG-1999; 11-AUG-1999;	09-AUG-1999;	06-AUG-1999;	05-AUG-1999; 06-AUG-1999;	05-AUG-1999;	04-AUG-1999;	02-AUG-1999; 03-AUG-1999;	02-AUG-1999; 02-AUG-1999;	27-JUL-1999; 28-JUL-1999;	27-JUL-1999; 27-JUL-1999;	23-JUL-1999; 26-JUL-1999;	23-JUL-1999; 23-JUL-1999;	22-JUL-1999; 22-JUL-1999;	22-JUL-1999; 22-JUL-1999;	21-JUL-1999; 21-JUL-1999;	20-JUL-1999; 21-JUL-1999;	20-JUL-1999; 20-JUL-1999;	19-JUL-1999;	19-JUL-1999;	19-JUL-1999; 19-JUL-1999;	19-JUL-1999;	16-JUL-1999;	14-JUL-1999; 15-JUL-1999;	12-JUL-1999; 13-JUL-1999;	08-JUL-1999;	06-JUL-1999;	01-JUL-1999;
30-AUG-1999; 31-AUG-1999; 01-SEP-1999; 07-SEP-1999;	27-AUG-1999; 27-AUG-1999; 27-AUG-1999;	25-AUG-1999; 26-AUG-1999; 27-AUG-1999	23-AUG-1999; 23-AUG-1999;	20-AUG-1999; 20-AUG-1999;	18-AUG-1999; 20-AUG-1999;	16-AUG-1999; 17-AUG-1999;	13-AUG-1999;	12-AUG-1999;	10-AUG-1999; 11-AUG-1999;	09-AUG-1999;	06-AUG-1999;	05-AUG-1999; 06-AUG-1999;	05-AUG-1999;	04-AUG-1999;	02-AUG-1999; 03-AUG-1999;	02-AUG-1999; 02-AUG-1999;	27-JUL-1999; 28-JUL-1999;	27-JUL-1999; 27-JUL-1999;	23-JUL-1999; 26-JUL-1999;	23-JUL-1999; 23-JUL-1999;	22-JUL-1999; 22-JUL-1999;	22-JUL-1999; 22-JUL-1999;	21-JUL-1999; 21-JUL-1999;	20-JUL-1999; 21-JUL-1999;	20-JUL-1999; 20-JUL-1999;	19-JUL-1999;	19-JUL-1999;	19-JUL-1999; 19-JUL-1999;	19-JUL-1999;	16-JUL-1999;	14-JUL-1999; 15-JUL-1999;	12-JUL-1999; 13-JUL-1999;	08-JUL-1999;	06-JUL-1999;	01-JUL-1999;
30-AUG-1999; 99US-01 31-AUG-1999; 99US-01 01-SEP-1999; 99US-01 07-SEP-1999; 99US-01	27-AUG-1999; 99US-01 27-AUG-1999; 99US-01 27-AUG-1999; 99US-01	25-AUG-1999; 99US-01 26-AUG-1999; 99US-01 27-AUG-1999: 99US-01	23-AUG-1999; 99US-01 23-AUG-1999; 99US-01	20-AUG-1999; 99US-01. 20-AUG-1999; 99US-01.	18-AUG-1999; 99US-01 20-AUG-1999; 99US-01	16-AUG-1999; 99US-01 17-AUG-1999; 99US-01	13-AUG-1999; 99US-01:	12-AUG-1999; 99US-01	10-AUG-1999; 99US-01 11-AUG-1999; 99US-01	09-AUG-1999; 99US-01	06-AUG-1999; 99US-01	05-AUG-1999; 99US-01 06-AUG-1999; 99US-01	05-AUG-1999; 99US-01	04-AUG-1999; 99US-01	02-AUG-1999; 99US-01 03-AUG-1999; 99US-01	02-AUG-1999; 99US-01 02-AUG-1999; 99US-01	27-JUL-1999; 99US-01 28-JUL-1999; 99US-01	27-JUL-1999; 99US-01 27-JUL-1999; 99US-01	23-JUL-1999; 99US-01 26-JUL-1999; 99US-01	23-JUL-1999; 99US-01	22-JUL-1999; 99US-01 22-JUL-1999; 99US-01	22-JUL-1999; 99US-01 22-JUL-1999; 99US-01	21-JUL-1999; 99US-01 21-JUL-1999; 99US-01	20-JUL-1999; 99US-01 21-JUL-1999; 99US-01	20-JUL-1999; 99US-01 20-JUL-1999; 99US-01	19-JUL-1999; 99US-01	19-JUL-1999; 99US-01	19-JUL-1999; 99US-01 19-JUL-1999; 99US-01	19-JUL-1999; 99US-01	16-JUL-1999; 99US-01	14-JUL-1999; 99US-01 15-JUL-1999; 99US-01	12-JUL-1999; 99US-01 13-JUL-1999; 99US-01	09-JUL-1999; 99US-01	06-JUL-1999; 99US-01	01-JUL-1999; 99US-01
1-AUG- 1-SEP- 7-SEP-	27-AUG-1999; 99US-01 27-AUG-1999; 99US-01 27-AUG-1999; 99US-01	25-AUG-1999; 99US-01 26-AUG-1999; 99US-01 27-AUG-1999: 99US-01	23-AUG-1999; 99US-01 23-AUG-1999; 99US-01	20-AUG-1999; 99US-01. 20-AUG-1999; 99US-01.	18-AUG-1999; 99US-01 20-AUG-1999; 99US-01	16-AUG-1999; 99US-01 17-AUG-1999; 99US-01	13-AUG-1999; 99US-01:	12-AUG-1999; 99US-01	10-AUG-1999; 99US-01 11-AUG-1999; 99US-01	09-AUG-1999; 99US-01	06-AUG-1999; 99US-01	05-AUG-1999; 99US-01 06-AUG-1999; 99US-01	05-AUG-1999; 99US-01	04-AUG-1999; 99US-01	02-AUG-1999; 99US-01 03-AUG-1999; 99US-01	02-AUG-1999; 99US-01 02-AUG-1999; 99US-01	27-JUL-1999; 99US-01 28-JUL-1999; 99US-01	27-JUL-1999; 99US-01 27-JUL-1999; 99US-01	23-JUL-1999; 99US-01 26-JUL-1999; 99US-01	23-JUL-1999; 99US-01	22-JUL-1999; 99US-01 22-JUL-1999; 99US-01	22-JUL-1999; 99US-01 22-JUL-1999; 99US-01	21-JUL-1999; 99US-01 21-JUL-1999; 99US-01	20-JUL-1999; 99US-01 21-JUL-1999; 99US-01	20-JUL-1999; 99US-01 20-JUL-1999; 99US-01	19-JUL-1999; 99US-01	19-JUL-1999; 99US-01	19-JUL-1999; 99US-01 19-JUL-1999; 99US-01	19-JUL-1999; 99US-01	16-JUL-1999; 99US-01	14-JUL-1999; 99US-01 15-JUL-1999; 99US-01	12-JUL-1999; 99US-01 13-JUL-1999; 99US-01	09-JUL-1999; 99US-01	06-JUL-1999; 99US-01	01-JUL-1999; 99US-01

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RESULT 13
AAZ46167
ID AAZ461
XX AAZ461
XX AAZ461
XX 16-MAY
XX 16-MAY
XX CDNA S
XX Human;
KW Human;
KW immune
XX immune
XX Human;
KW immune
XX FH Key
FT CDS
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Best Local S
Matches 42
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14-OCT 1999
14-OCT 1999
14-OCT 1999
11-OCT 1999
21-OCT 1999
21-OCT 1999
21-OCT 1999
21-OCT 1999
21-OCT 1999
22-OCT 1999
22-OCT 1999
22-OCT 1999
25-OCT 1999
25-OCT 1999
25-OCT 1999
26-OCT 1999
26-OCT 1999
26-OCT 1999
27-OCT 1999
28-OCT 1999
28-OCT 1999
28-OCT 1999
29-OCT 1999
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24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
07-OCT-1999;
                                                                              Human;
immune
                                                                                                                          cDNA sequence encoding a human phosphorylation effector PHSP-30:
                                                                                                                                                            16-MAY-2000
                                                                                                                                                                                                                        AAZ46167 standard;
                                                                                                                                                                                           AAZ46167;
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14-OCT-1999
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||| ||
                                                sapiens.
                                                                                                                                                                                                                                                                                                        ACCACCAC
                                                                                                                                                                                                                                                                                                                                                                                   cgagggctgcactgactggtaagftfcacatgtaaggtgatacttatcttcaatttattc
                                                                                                                                                                                                                                                                                                                                                                 CGATGGCTCCTCTGACTGGGAGGTTCTTCCTTGCGGGTTGTTCTTCCCCCAACAATTTCTTC
                                                                              phosphorylation effector; PHSP; proliferative disorder; disorder; neuronal disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                             ch 21.5%; l Similarity 61.8%; 42; Conservative
                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                      870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9908-0156458
9908-0157753
9908-0157753
9908-0158232
9908-0158233
9908-0158233
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9908-0158233
9908-0159294
9908-0159294
9908-0159233
9908-0159331
9908-0159637
9908-0159638
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9908-0160760
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   Location/Qualifiers 62..1132
                                                                                                                                                                                                                        CDNA; 2347
                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 26.4; Di
; Pred. No. 8.8;
0; Mismatches
                                                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                            .
8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1474;
                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                              114
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              Homo sapiens
                                           Human; primer;
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RESULT 14
AAH15633/c
                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-1998;
14-OCT-1998;
03-NOV-1998;
19-NOV-1998;
22-DEC-1998;
12-JAN-1999;
12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ46138-Z46168 encode human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, lumnune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human phosphorylation effectors useful for the diagnosis, treatment and prevention of proliferative, immune and neuronal disorders \, -
   Human
                                   26-JUN-2001
                                                                                                      AAH15633 standard; cDNA; 2620 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 141-142; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patterson C, Banc
Reddy R, Lu DAM,
                                                                      AAH15633;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2347 BP; 745 A; 442 C; 454 G; 706 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-1999;
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                                                                                                                                                                                              94
                                                                                                                                                                                                                              68
                                                                                                                                                                                                                                                                34
                                                                                                                                                                                                                                                                               agatgaaaaataccttcaagctat 117
                                                                                                                                                                                                          aggtgatacttatcttcaatttat 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-183125/16.
DB; AAY68798.
                                                                                                                                                                                                                                                              increased PHSP expression/activity.
   CDNA
                                                                                                                                                                                                                                                                                                                                     48;
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sequence SEQ ID NO:13969
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lal P, Tang YT,
Bandman O, Au-
DAM, Shih LL;
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0123494.

98US-0152814.

98US-0173482.

98US-0106889.

98US-0109093.

98US-0113796.

99US-0173482.

99US-0229005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "phosphorylation effector"
                                                                                                                                                                                                                                                                                                                                                   21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INC.
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Au-Young J,
                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                   Score 26.4;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                     Mismatches
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Gorgone
                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guegler
gone GA,
                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                   Length
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Yue
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H, Azimzai
                                                                                                                                                                                                                                                                                                                                                                     2347;
                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                  93
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detection; diagnosis; antisense therapy; gene therapy;

SS

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RESULT 15
AAX20838
ID AAX208
XX
AC AAX208
XC AAX208
XX
DT 05-MAY
XX
                                                                                                                                 В
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                                                                                                                                                                                   Вb
                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                       The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary cto the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination cof an oligonucleotide which comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a polynucleotide which comprises a 3'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in companies at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in companies at least 15 nucleotides and the combination of the fragy and sequence is selected from those defined in companies are useful for synthesising polynucleotides, companies are useful for synthesising polynucleotides, companies and companies are useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are useful for the companies of the abnormality of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13674 represent human cDNA sequences; and AAH3628 to AAH13632 represent oligonucleotides, all of which are used in the exemplification.
                                                                                                                                                                                                                                                  Query Match
Best Local 9
                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
             05-MAY-1999
                                                                                                                                   1279
                                                                                                                                                                                    1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ota T, Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota
                                        AAX20838;
                                                                AAX20838
                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID 13969;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              full-length cDNAs
                                                                                                                                                          65
                                                                                                                                                                                                             Ŋ
                                                                                                                                              actgactggtaagtttcacatgtaaggtgatacttatcttcaattt 110
                                                                                                                                                                                                  tattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgc 64
                                                                                                                                                                                   TAGAGCACAGGAGAAAGGTCTTAAAACCCTGGGCTTATGGGACGTTACCACGGAGACTGC 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-318749/34.
                                                                                                                              ACAGAGTGAGAAGATCCATTTTAAAGCTGATGATGAATAATATTTT 1234
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T,
Sugiyama
                                                                                                                                                                                                                                                                                                       2620
                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                      Conservative
             (first
                                                                                                                                                                                                                                                                                                     вP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000EP-0116126
                                                                                                                                                                                                                                                                                                       788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INST
                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishikawa T,
T, Wakamatsu
            entry)
                                                                                                                                                                                                                                                 21.1%; 52.8%;
                                                                                                                                                                                                                                                                                                     A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2537pp + CD ROM;
                                                                634
                                                                                                                                                                                                                                                                                                     581
                                                                                                                                                                                                                                  Score 26; DB Pred. No. 15; 0; Mismatches
                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                   Ü
                                                                                                                                                                                                                                                                                                     456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                    G;
                                                                                                                                                                                                                                                 DB
15;
                                                                                                                                                                                                                                                                                                     795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                     T; 0
                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito K,
Ctsuki
                                                                                                                                                                                                                                     50;
                                                                                                                                                                                                                                                             Length 2620;
                                                                                                                                                                                                                                                                                                     other;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto
                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                          ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treponema
                                                                                                                                                                                                                                                                                                                                                                                   348
                                                                                                                                                                                                                                                                                                                                                         109
                                                                                                                                                                                                                                                                                                                                                                                                            49
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RESULT 16
AAV52156/c
ID AAV52156;
XX
AC AAV52156;
XZ
AC AAV52156;
XX
DT 23-OCT-1998 (first entry)
XX
DE Streptococcus pneumoniae genome
XX
Computer readable medium; vacci
XX
PN W09818931-A2.
XX
PD 07-MAY-1998.
XX
PF 30-OCT-1997; 97WO-US19588.
XX
PR 31-OCT-1996; 96US-0029960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARX20500-21243 represent polynucleotide sequences from the genome Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidu infections, particularly syphilis. They can also be used for detections are related to Borrelia infections in animals, and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Treponema pallidum nucleic acids - used to products for the detection, diagnosis, characterisation, and therapy of T. pallidum infections, particularly syph.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 929; 1150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 634 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09859034-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide sequence from the genome of Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 atat 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttat 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gctatgagaattctgcactttctactcaattttacttggaaactcaaactgttctaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gcaatgcgagggctgcactgactggtaagtttcacatgtaaggtgatacttatcttcaat 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-081273/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                               pneumoniae genome fragment SEQ ID NO:23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0050667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US13041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 A; 127 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection; syphilis;
ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.8%;
                                                                                                                                                                                            S. pneumoniae; genome; uruy.....vaccine; pharmaceutical composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25.6; D
Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 G; 155 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection; animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tion, prevention syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
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/note= " CDS 179421	FH Key Location/Qualifiers FT CDS 3891579 FT /*tag= a	OS Helicobacter pylori XX	<pre>vaccine; treatment; duodenal; gastric ulcer; active adenocarcinoma; ss.</pre>	<pre>ce factor; exporter molecu s; VIR B4; Agrobacterium t strain; virulence; diagnos</pre>	DE CagI locus.	DT 30-JUN-1997 (first entry)	AA AAT46159;	ID AAT46159 standard; DNA; 19932 BP.	RESULT 17	Db 219 CAACTATGAGGAACTGATGGCGCAAGGTGGCTTCTACGCTGACTTGTA 172	28 caaccctgatgacctaatggcgcaatgcgagggctgcactgactg	; Conservative	Query Match 20.8%; Score 25.6; DB 19; Length 7147; Best Local Similarity 70.8%; Pred. No. 29;	SQ Sequence 7147 BP; 2088 A; 1641 C; 1265 G; 2153 T; 0 other;	pharmaceutical compositions and vaccines for S. pneumoniae.	expression modulating fragments of the S. pneumoniae genome. Profession the present invention can be used in diagnosis kits and ass		CC primers derived from the fragment of the S. pneumoniae genome to prime CC the amplification and isolating the amplified sequences. The computer				CC fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the		ide		The	PS Claim 1; Page 289-293; 1409pp; English.	pneumoniae	PT Computer readable medium with recorded Streptococcus pneumoniae PT polynucleotide sequences - useful in diagnostic kits and assays, and PT pharmaceutical compositions and vaccines for Streptococcus	WPI; 1998-272225/24.	Kunsch CA, Rosen CA;	HUM SC.
FT CDS	FT CDS	97 P	FT CDS	FT CDS	ਸ਼ੵਸ਼	FT CDS	P P P	FT CDS	FT	FT CDS		FT CDS	FT CDS		FT CDS	ਜ਼ ਜ਼ ਜ਼	FT CDS	FT.	FT CDS	д Б;	FT CDS	FT	FT CDS	FT.	FT CDS			FT CDS	FT CDS	FT T	FT CDS	FT T
given" (1386614129)	<pre>complement (1337413742) /*tag= r /note= "putative open reading frame; no start codon</pre>	/"cdg" q /note= "putative open reading frame; no start codon given"	given" ment (1274313420)	1055712758  /*tag= p /note= "putative open reading frame; no start codon	/ncte= "putative open reading frame; no start codon /note= "putative open reading frame; no start codon	<u>е</u>	/*tag= n /note= "putative open reading frame; no start co	₽	<pre>/*tag= m /note= "putative open reading frame; no start codon</pre>	given" nt (84968918)	<pre>/*tag= 1 /note= "putative open reading frame; no start codon</pre>	given" ment (79758454)	<pre>complement (73717802)  /*tag= k /note= "putative open reading frame; no start codon</pre>	<pre>/note= "putative open reading frame; no start codon</pre>	complement (70077375) /*tag= j	=	complement (65627074)		complement (62186613)	-	complement (55086233) /*tag= h	-	complement (30203259) /*tag= q	<pre>/note= "putative open reading frame; no start codon</pre>	nt (25913001) f	given"	(+::co.ex.c)	given"  1778 2173	44885426  /*tag= d  /note= "multative open reading frame: no start codon	<pre>/note= "putative open reading frame; no start codon given"</pre>	33434491 /*tag= c	<pre>/*tag= b /note= "putative open reading frame; no start codon</pre>

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RESULT 1
AAZ88746
ID AAZ8
XX
AC AAZ8
AC AAZ8
AC AAZ8
AX
AC AAZ8
                                                                                                                                                                 Qy
                                                                                                                                                                                          Вb
                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                       CC The present sequence is the complete nucleotide sequence of the CayI C locus, including the true 5'-terminus of CayI. The sequence was CC constructed using overlapping clones (one of which also overlaps with CC the CayA region). The CayI region contains clusters of putative open CC reading frames (ORFs) with different polarities. The putative ORFs for CC this region are shown above. It is hypothesised that some of these ORFs CC may encode exporter molecules with homology to the ptl genes of CC Bordetella pertussis and VIR B4 genes of Agrobacterium tumefaciens and CC for proteins with motifs shared by the purported invasion factors of CC Salmonella genus. The absence of the CayA gene in the type I strains is Cassociated with the absence of CayI sequences (which may encode virulence CC factors restricted to type I strains). The CayA gene in the type I strains is Cassociated with the absence of CayI sequences (which may encode virulence CC factors restricted to type I strains). The CayA gene in the diagnosis of H. pylori CC (claimed) for the treatment of H. pylori infection associated with e.g. CC (claimed) for the treatment of H. pylori infection associated with e.g. two
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                          8085
              A. dichotoma
                                     18-MAY-2000
                                                                                                                                             8145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori CagI polynucleotide and related proteins in diagnosis and in vaccines for the treatment of H. pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
20-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                            AAZ88746;
                                                                                   AAZ88746 standard; DNA; 591
                                                                                                                                                                                                                                                                                               Sequence 19932 BP; 6677 A;
                                                                                                                                                                                                                                                                                                                      gastritis) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 3A-R; 303pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Covacci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9633274-A1
                                                                                                                                                                                                                                                                                                                                   duodenal and gastric ulcers, severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOC-) BIOCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection associated disease
                                                                                                                                                                   71
                                                                                                                                                                                                     11 aaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcactgac 70
                                                                                                          18
                                                                                                                                                        1996-485780/48.
DB; AAW06930-50.
                                                                                                                                          cgttaaattcccctgttaatttgctaatatttaagatattgttccccacagc
                                                                                                                                                                                        aaatgcttgcaatctgactattaacagcaccaatttgcgcgccttggctgttgccttgag
                                                                                                                                                                                                                                          58;
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                        Conservative
             kabutosin A DNA
                                    (first entry)
                                                                                                                                                                                                                                                                                                                      gastric adenocarcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0477451
95US-0425194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-IB00343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (19296..19832)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                 20.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "putative open reading given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "putative open reading given"
                                                                                                                                                                                                                                                                                               3635 C; 3483 G;
                                                                                   ВP
                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                  Score 25.6;
Pred. No. 4:
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                   forms of active
                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                              DΒ
                                                                                                                                                                                                                                                                                               6137
                                                                                                                                                                                                                                       54;
                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 frame;
                                                                                                                                                                                                                                                                                               Η;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                             Length 19932;
                                                                                                                                                                                                                                                                                                                                 gastritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  start codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    start codon
                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                (esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                       0;
RESULT 19
AAH17997/c
ID AAH179
XX AAH179
AC AAH179
AC AAH179
XX
DE Human
XX
Human;
XX
Homo s
XX
EP1074
XX
PN EP1074
XX
PD 07-FEB
XX
PR 28-JUL
XX
28-JUL
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                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                           Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
 29-JUL-1999;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes two novel peptides which have antibacter: activity, designated kabutosin A and B and which have been isolate Allomyrina dichotoma. The peptides are used as food preservatives and medical antibacterial agents. This sequence encodes the A. dichotoma kabutosin A protein described in the method of the
                               07-FEB-2001
                                                                                                                       Human; primer;
28-JUL-2000;
                                                              EP1074617-A2
                                                                                           Homo sapiens
                                                                                                                                                      Human cDNA sequence SEQ ID NO:17797.
                                                                                                                                                                                      26-JUN-2001
                                                                                                                                                                                                                    AAH17997;
                                                                                                                                                                                                                                                   AAH17997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 9-10; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A new peptide, an antibacterial agent, a new peptide gene, recombinant DNA and preparation of a new peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-176990/16.
P-PSDB; AAY51547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP2000026499-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allomyrina dichotoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kabutosin A; kabutosin B;
medical; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NORQ ) NORINSUISANSHO SANSHI
(NODA ) ZH NODA SANGYO KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2000
                                                                                                                                                                                                                                                                                                                              359
                                                                                                                                                                                                                                                                                                                                                                                         299
                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                       23
                                                                                                                                                                                                                                                                                                                            cctctaatgttgaac
                                                                                                                                                                                                                                                                                                                                                         catgtaaggtgatac
                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 183 A; 123 C;
                                                                                                                                                                                      (first entry)
                                                                                                                         detection; diagnosis; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0197190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98JP-0197190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 82..516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "kabutosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                   CDNA; 2333 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.7%;
                                                                                                                                                                                                                                                                                                                                                           97
                                                                                                                                                                                                                                                                                                                              373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial; food preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25.4;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KONCHU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   · Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                         gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from
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RESULT 20
AAA92497
ID AAA924
XX
AC AAA924
XX
DT 17-JAN
XX
DE Haemop
XX
KW Hia; a
KW non-ty
KW antiba
KW diagnc
XX
KW diagnc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at 1'-end sequence, where the CC chief of the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC the full-length cDNAs. The primers allow obtaining of the full-length CC CNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH3633 to AAH18742 represent human cDNA sequences; AAB92446 to CC CAAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification CC of the present invention.
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                                                                                                                                                                                                                                                                                                                                 Ω
                                                                                                                                                                                                                                                                                                                                                                      망
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 47; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                      1487
                                                                                                                                                                                                                                                                                                                                                                        1547
                non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen; ds.
                                                                                                                                         17-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                  Hia; adhesin;
                                                                                                                                                                            AAA92497;
                                                                                                                                                                                                             AAA92497 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length CDNAs defined in the specification. Where a primer set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and/or diagnosis of the full-length cDNAs -
                                                                                                      Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                                                                                                                                                                                                                                                                                                                                                              TAAGCTGAAGGTCAGATTCAAAT 1465
                                                                                                                                                                                                                                                                                                                        taaggtgatacttatcttcaatt 109
                                                                                                                                                                                                                                                                                                                                                                      ACTGCACAGACCCTGTACTGGCACAAGTTGATGGGTCCACTGGAAAAGAAATGCCCAAATA 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID 17797; 2537pp + CD ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugiyama T,
                                                                                                     influenzae adhesin (Hia) gene from NTHi strain K9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                         (first
                                                                Haemophilus influenzae adhesin; NTHi; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 699 A; 427 C; 416
                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nishikawa T,
                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25.4; DF Pred. No. 24; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G; 791 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2333;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       86
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RESULT 21
AAH83942/c
ID AAH839
XX AAH839
XY AAH839
XY CAH11t
XX CAH11t
XX Olfact
KW Olfact
KW Olfact
KW Olfact
XX Aromas
XX CAH11t
XX X
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                                                                                                                                                                                                                                                                                                                                                   Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC gene from the non-typeable Haemophilus influenzae (NVHi) strain k9.

CC Hia genes and proteins have antiinflammatory, auditory and antibacterial cc activities, and can be used in the production of a vaccine. An CC immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing CC protection against disease caused by Haemophilus strains in a CC susceptible host, preferably a human. An Hia protein is useful as an CC antigen, in immunogenic preparations including vaccines, as a carrier CC for other immunogens, and in the generation of diagnostic reagents. Hia CC is useful for treating diseases caused by the infection of Haemophilus CC influenzae such as meningitis, epiglottitis, septicaemia and otitis CC media. Recombinant production of Hia favours high recovery of the protein compared to the low recovery of native protein from Haemophilus CC influenzae species. A truncated protein has a significantly higher CC amount of recovery than a full-length protein.
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                          Callithrix jacchus
                                                                                       Olfactory receptor;
                                                                                                                    Callithrix jacchus olfactory receptor encoding gene 10
                                                                                                                                                                                AAH83942;
                                                                                                                                                  25-SEP-2001
                                                                                                                                                                                                              AAH83942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3300 BP; 1099 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a Haemophilus influenzae adhesin (Hia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 22; 275pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid e
use as antigens and
infection :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-618897/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Loosmore SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-2000; 2000WO-CA00289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200055191-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CONN-) CONNAUGHT LAB
                                                                                                                                                                                                                                                                                                      117 cacaaca
                                                                                                                                                                                                                                                                                        214 gccaata
                                                                                                                                                                                                                                                                                                                                                 154 agtgcttctgttacgagtaggttgaatgtttatggcgatacgaatactaaattcaatgca 213
                                                                                                                                                                                                                                                                                                                                                                    57 agggctgcactgactggtaagtttcacatgtaaggtgatacttatcttcaattttattcca 116
                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                         perfumery;
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                              standard; DNA; 649
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                      123
                                                                                                                                                                                                                                                                                         220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0268347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding 
d vaccines
                                                                       primate; mouse;
toxic substance;
                                                                                                                                                                                                                                                                                                                                                                                                                            20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          606 C;
                                                                                                                                                                                                              ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hemophilus influenzae adhesin protein, and for treating Hemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25.4;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MH;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          819
                                                                          human;
ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G; 776 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                             DΒ
                                                                                       food processing industry;
                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other;
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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WO200146262-A2

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RESULT 2
AA160262
ID AA16
XX AA16
XX Huma
XX Huma
XX Huma
KW Perii
KW A1zi
KW A1zi
KW Leul
XX Leul
XX Hom
XX PN WO2
XX Hom
XX FR S6-1
XX PR 25-1
PR 25-1
PR 09-1
PR 19-1
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                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 42
21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                              Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening, artheitic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to olfactory receptors (AAG98432-AAG98609) and the genes encoding them (AAH83879-AAH84131) including pseudogenes of 10 primate species, mouse and human. The nucleic acids and receptors may be used in the food processing industry (e.g. for the detection of aromas, quality control and sample analysis), in perfumery (e.g. for the analysis or comparison of perfumes) and in the environment (e.g. for the detection of toxic substances and/or trapping of odours).
                                                                                                  WO200153312-A1
                                                                                                                     Homo
                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy;
peripheral nervous system; neuropathy; central nervous system;
                                                                                                                                                                                                        Human polynucleotide
                                                           26-DEC-2000;
                                                                               26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids
for analysis o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-DEC-1999;
21-DEC-2000;
                                                                                                                                        leukaemia;
                                                                                                                                                                                                                            22-OCT-2001
                                                                                                                                                                                                                                              AAI60262;
                                                                                                                                                                                                                                                                 AAI60262 standard; cDNA; 3684 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rouquier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CNRS )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-2001
                                                                                                                                                                                                                                                                                                                                                       271
                                                                                                                                                                                                                                                                                                                 211
                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                                                                                                                                                                                   CAGGGAATGTAGGTGGGAGATGCTGCAAGAACCCAATAGCATGAGTAGGCAATGCCGGGG
                                                                                                                     sapiens.
                                                                                                                                                                                                                                                                                                                 GTTCATAGCC
                                                                                                                                                                                                                                                                                                                                  ctgcactgac
                                                                                                                                                                                                                                                                                                                                                                       caggtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgaggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-381911/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG98470.
                                                                                                                                                                                                                                                                                                                                                                                                                                           649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                        SS
           2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s encoding primate and murine olfactory receptors, useful odours e.g. in food processing and perfumery -
                                                           2000WO-US34263
                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CENT NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Giorgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0171746.
2000US-0747155.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150-151;
                                                                                                                                                                                                                                                                                                                                   70
                                                                                                                                                                                                                                                                                                                                                                                                                                          126 A; 192 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ū
                                                                                                                                                                                                                                                                                                                                                                                                   20.5%;
                                                                                                                                                                                                        SEQ
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                                                                                                                                                                                                        IJ
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                                                                                                                                                                                                        Ö
                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                         4251.
                                                                                                                                                                                                                                                                                                                                                                                                                                          139 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    25.2; I
                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                               649;
                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                      212
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                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                         В
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           WO9625519-A1
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AATT33537
ID AATT3
XX
AC AATT3
XX
T15-F
XX
DE BCG
XX
BCG
KW MYCC
XX
FH Key
FT misc
FT
XX
PN WO9(
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                           3183
                                                                                                                                                                                                                                                                                                                                                           3123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang
Wang
                                                                misc_feature
                                                                                                     Mycobacterium
                                                                                                                              mycobacteria;
                                                                                                                                                                     BCG deletion
                                                                                                                                                                                                                      AAT33537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2000; 2000US-0662191
19-OCT-2000; 2000US-0693036
29-NOV-2000; 2000US-0727344
                                                                                                                                                                                             15-FEB-1998
                                                                                                                                                                                                                                            AAT33537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.N.S disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-)
                                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                                                                                                                   23
                                                                                                                                            delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                          actagtcaaatagattcttcaactcaaaatatctcacacaac
                                                                                                                                                                                                                                                                                                                                cacatgtaaggtgatacttatcttcaatttattccacacaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   γŢ,
QA,
                                                                                                                                                                                                                                                                                                                                                         tgcaatgcaacccccatgtcctctgtccccaaagctaccactttaaagttcaacttttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-442253/47.
DB; AAM41106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acids and
as central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence
                                                                                                                                                                                                                                                                                                                                                                                                               54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
                                                                                                                                            ω
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                              virulence;
; vaccine; ;
                                                                                                                                                                  region
                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                      bovis strain
                                                             Location/Qualifiers 1406..10673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO 4251; 10078pp;
                                                   /*tag=
                                       note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           970
                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goodrich R,
                                                                                                                                                                  3 and flanking sequences
                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         20
52
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                                       "BCG
                                                                                                                               infection;
                                                                                                                                                                                                                                                                                                                                                                                                                         . 5%;
                                                                                                                                           avirulence; attenuation;
                                                                                                                                                                                                                                             12412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides, useful
system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           818
                                                                                                      BCG
                                                                                                                                                                                                                                                                                                                                                                                                         Score 25.2; DI
Pred. No. 33;
0; Mismatches
                                       delta
                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 this
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Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ç
                                                                                                                                                                                                                                             ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patent
                                       L
                                                                                                                               marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                        25.2; I
                                      deletion region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ma
Xue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 did
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                                                                                                                               SS
                                                                                                                                                                                                                                                                                                                                                                                                                                      DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not
                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                    122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 form
                                                                                                                                           gene deletion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ren F,
Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                      3684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               printed
                                                                                                                                                                                                                                                                                                                                                             3182
                                                                                                                                                                                                                                                                                                                                                                                    80
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RESULT 24
AAH32402/c
ID AAH324
XX AAH324
XX AH324
XX Human
DT 30-JUL
XX Human
XX Human;
KW Second
KW Secont
XX Homo S
XX WO2001
XX WO200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This DNA sequence comprises Mycobacterium bovis BCG deletion Sequence BCGdelta3. A specific genetic deletion of this region C results in an avirulence phenotype of the mycobacterium. 2 Other C deletion regions (see AAT3535 and AAT33536) have also been detected. C Identification involved screening a BCG cosmid library with a CC radiolabeled probe obtained following DNA subtraction between CC virulent Mycobacterium tuberculosis H37Rv and avirulent BCG.

CC The deletions provide useful markers for the identification of an CC avirulent, or a virulent, mycobacterial phenotype. Determination CC avirulence requires the detection of the presence or absence of CC the deletion; the deletions are detected either by detecting the presence or absence of deletion junctions (see AAT33538-46), or by CC detecting the presence or absence or absence of the sequences contained within CC the deletion. Deletion polypeptides are used as components of CC immunological assays and in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                           08-OCT-1999; 99US-0158615.
24-FEB-2000; 2000US-0184809.
                                                                                                                                                                                                                                                                                                       Human; olfactory receptor; OR;
secondary scent determination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5990 gacatggctttcaacgccgatgtcggtatggcgacctgcaaacgctgtggtgac 6043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect
                                                                                                                         06-OCT-2000; 2000WO-US27582.
                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                Human olfactory receptor polynucleotide, SEQ ID NO: 975
                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH32402 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mahairas GG,
(DIGI-) DIGISCENTS.
(YEDA ) YEDA RES &
                                                                                                                                                                 19-APR-2001
                                                                                                                                                                                                   WO200127158-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 3; 66pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PATH-) PATHOGENESIS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 gagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcactgac 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 36; Conserv
                                                                                                                                                                                                                                                                                    profile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12412 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stover CK;
                                                                                                                                                                                                                                                                                    t determination; polypeptide library; odour r scent fingerprint; scent representation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0390878
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  & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2146 A; 4273 C; 3876 G; 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25.2;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                            primary scent determination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 other;
                                                                                                                                                                                                                                                                                                     receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                       CDS
                   US5861498-A
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Similarity

20.3%;

Score Pred.

No.

DB 24;

22;

Length

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receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create
                                                                                                                                                                                                                                                                                              scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour
                                                                                             and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties
                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 569; 1857pp; English
Sequence 933
                                                                 of different individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bellenson
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   B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith D,
   206
Α;
   267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lancet D,
Ç
187 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glusman G,
   273
   T; 0
   other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fuchs T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yanai I;
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polyA_signal
                                                    polyA_signal
                                                                              polyA_signa
                                                                                                       polyA_signal
                                                                                                                                                                                    Spodoptera frugiperda
                                                                                                                                                                                                             transplant;
                                                                                                                                                                                                                                                                               27-APR-1999
                                                                                                                                                                                                                                                                                                         AAX0441;
                                                                                                                                                                                                                                                                                                                                  AAX04441 standard; cDNA;
                           polyA_signal
                                                                                                                                                                                                                          Immunophilin; moth; insect cell; nuclear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     474
                                                                                                                                                                                                                                                                                                                                                                                                  414 TTTCA 410
                                                                                                                                                                                                                                                                                                                                                                                                                           61 ctgca 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 caggtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgaggg
                                                                                                                                                                                                                                                  frugiperda immunophilin FKBP46 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGGAATGTAGGTGGGAGATGCTGCAAGAACCCAATAGCATGAGTAGGCAATGCCATGG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                             tissue graft;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                             (first entry)
                                          1868..1873
                            /*tag=
2052..2
                                                                  1850..1855
/*tag= c
                                                                                                        /product=
1764..1769
                                                                                                                                                160..1398
                                                                                                                                                            Location/Qualifiers
                                                                                          /*tag=
                                                                                                                                  /*tag=
                ĭ.2057
g= e
 .2242
                                                                                                                                                                                                                                                                                                                                   2284
                                                                                                                                                                                                               ds
                                                                                                                      "immunophilin FKBP46"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                          immunosuppression; drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 26
AAX23518/c
ID AAX235
AC AAX235
XX AMINOP
AC AMINOP
KW Prenat
KW Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prenatal diagnosis; angioedema; antihypertensive agent; atherosclerosis; arterial stenosis; industrial protein feed; malabsorption syndrome; proteinaceous waste degradation; additive; immunohistochemistry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1755
                                                                                                                                                                                                                                                                  02-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09911799-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the cDNA encoding the immunophilin FKBP46 from the moth Spodoptera frugiperda. FKBP46 is a novel insect cell nuclear immunophilin, which can be used to study and identify additional immunosuppressive drugs that bind to it. Such immunosuppressive agents
                                                                                                               Ryan JW,
                                                                                                                                                                                                                                                                                                                                           02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aminopeptidase; human; AmP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX23518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX23518 standard; DNA; 49998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressive drugs that bind to it. Such immunosuppress can be used in treating transplant and tissue graft patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agents
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31-OCT-1996;
                                                                                                                                                                                        (MEDI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cactgactggtaagtttcacatgtaaggtgatacttatcttcaat 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-130433/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
55; Conserv
                                                                                                                                                                                        MEDICAL COLLEGE GEORGIA RES
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                                                                                                               Sprinkle TJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                  97US-0057854.
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96US-0741134.
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52.4%;
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                                                                                                                   Venema RC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; treatment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes the isolation of a novel human aminopeptidase PC (Amp). This protein is used to produce recombinant Amp and can be used for gene therapy for treating Amp-deficiency conditions. Its fragments are used as primers and probes to identify patients with homozygous and heterozygous Amp deficiency, including prenatal diagnosis (patients defective in Amp are at risk of developing angloedema if treated with angiotensin-converting enzyme inhibitors), also as antisense inhibitors in cases of excessive Amp expression. The product of the invention is also used to identify Amp-expressing sequences in other animals and to generate transgenic animals, and comparisons of genomic sequences are used to detect mutations. Amp inhibitors are potentially useful as antihypertensive agents and to prevent or treat arterial (re)stenosis or atherosclerosis. The structure of Amp is used to design synthetic substrates, e.g. for use in Amp assays. Amp, which hydrolyzes N-terminal imido bonds, can be used to degrade industrial protein feeds to free amino acids, to degrade protein synthems and for studying its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                  29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                          Ota T, :
Ishii S,
                                                                                      (HELI-) HELIX RES INST.
                                                                                                                                                                                                            28-JUL-2000;
                                                                                                                                                                                                                                          07-FEB-2001
                                                                                                                                                                                                                                                                        EP1074617-A2
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                  Human; primer;
                                                                                                                                                                                                                                                                                                                                                              Human cDNA clone (3'-primer) SEQ ID NO:9963.
                                                                                                                                                                                                                                                                                                                                                                                                                            AAH13128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH13128 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biological role. Antibodies against \mathsf{AmP} are used in immunohistochemical methods to study \mathsf{AmP} distribution.
                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49998 BP; 12605 A; 11725 C; 11351 G; 14317 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 109-139; 201pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding human aminopeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGTCAAATGCTCTAGTGATTGGGCCCCTT 42353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tggtaagtttcacatgtaaggtgatactt 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATGTCAGAGGCCTCAGAGCATTAATCACCACAGGTAGCCAAGCCTGGGGGGAAGAGGC 42382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcactgac
                                        Isogai T,
, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                  99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                              2000EP-0116126
                                                                                                                                                                                                                                                                                                                                  detection; diagnosis; antisense therapy; gene therapy;
                                          Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          528
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Pred.
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                                          Hayashi K,
A, Nagai K,
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95;
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                                          Saito K,
Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 49998;
                                            H
                                                           Yamamoto
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RESULT 2
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KW Prot
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XX meta
XX Arab
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Best Local S
Matches 41
    25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                                                                                                                            Hybridisation assay; genetic protein identification; signa metabolic pathway; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 1-east 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and the comprises as a sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and the comprise of the sequence is selected from those defined in the specification.
                                                                                                                                   25-FEB-2000;
                                                                                                                                                                          06-SEP-2000
                                                                                                                                                                                                                    EP1033405-A2
                                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC39501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC39501 standard; DNA; 1448
                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana DNA fragment SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                 2000EP-0301439
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99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
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on; signal transduction pathway;
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RESULT 29
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Shimkets
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RESULT 3
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proteins AAB49649 - AAB49658. Sequences AAF23420 - AAF23450 represent
primers and probes used in the isolation and characterisation of the SECX
DNA sequences of the invention. The new polypeptides and nucleic acids
can be used in screening assays, detection assays, preventive or
predictive medicine, therapeutic and prophylactic treatment, and
pharmacogenomics. Specifically, the SECX polypeptides and nucleic acids
care useful for treating cancer; other disorders related to angiogenesis
ce.g. abnormal wound healing, psoriasis; neurodegenerative diseases;
immune disorders; liver cirrhosis; benign tumours; fibrocystic conditions
and tissue hypertrophy (e.g. benign prostatic hypertrophy); allergic
reactions and conditions such as asthma and other respiratory problems;
crastalesses associated diseases or disorders. The
coplypeptides can also be used for bone, cartilage, tendon, ligament
and/or tissue growth or regeneration, wound healing, tissue repair and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA sequence SEQ ID NO:15679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH16592 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New SECX polypeptides and nucleic acids useful for treating or preventing cancer, other disorders related to angiogenesis, neurodegenerative diseases, autoimmune disorders and allergic reactions
                                                                                                                                                                            07-FEB-2001
                                                                                                                                                                                                                                   EP1074617-A2
                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                      Human; primer;
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P-PSDB; AAB49653.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clinical testing procedure, treat proliferative disorders including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replacement, gut protection or regeneration, as a contraceptive, to inhibit thromboses, infections caused by bacteria, virus, fungi and other
                                                                                                                   28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parasites, and as a vaccine. SECX antibodies may be used to isolate or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       letect SECX proteins, monitor protein level in tissue as part of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569 TCTGGCTCATTTAGAAAGGGATGATCATCTTCAAGATGTT 530
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                                                                                                                                                                                                                                                                                             sapiens
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99JP-0248036.
99JP-0300253.
2000JP-0118776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              benign hyperplasias.
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                                                                                                                   2000EP-0116126
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                                                                                                                                                          the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                           to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 \, \mathrm{full}-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899
                                                                                                  Sequence 1970 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID 15679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-318749/34.
                                                                                                                                           of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprises:
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                   Similarity
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, Sugiyama T, Wakamats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t invention describes primer sets for synthesising 5602 h cDNAs defined in the specification. Where a primer set (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                    434 A; 538 C;
                 20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wakamatsu
0;
                 Score 24.8;
Pred. No. 37;
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                                                                                                    G; 446 T;
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  27;
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                                                                                                    other;
                                        Length
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                                        1970;
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RESULT 31
AAQ80535
ID AAQ805
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Paralichthys olivaceus
                                                   transglutaminase; fish;
                                                                                                                         31-MAY-1996
                                                                                                                                                            AAQ80535
                                                                                                                                                                                               AAQ80535 standard; cDNA to mRNA; 2064
                                                                                                                                                                                                                                                                                                                                                        1876 cctcgaagacgttgtgcctcacagcgaggcctacaagggatgggaacttttatttcaaaa 1935
                                   Theragra chalcogramma;
                                                                                      Paralichthys olivaceus transglutaminase gene
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                                                                                                                                                                                                                                                                                                                                                                            gtgatact 98
                                                                                                                         (first entry)
                                   Paralichthys
                                                       recombinant
                                   production; Pagrus major;
olivaceus; Oncorhynchus keta;
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                                                                                                                                                                             A fish-originated trans:glutaminase amounts at low economic cost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The DNA encodes a protein, isolated from Paralichthys olivaceus, which has transglutaminase (TG) activity. The TG's of the invention can be isolated from Pagrus major, Theragra chalcogramma, Paralichthys olivaceus or Oncorhynchus keta. Fish-originated TG's are economical to produce in large quantities.
                                                                                                 Claim 10; Page 49; 94pp; Japanese.
                                                                                                                                                                                                                                                                                      WPI; 1995-100948/14.
P-PSDB; AAR65330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transglutaminase; fish;
Theragra chalcogramma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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                                                                                                                                                                                                                                                                                                                                                                                               (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paralichthys olivaceus transglutaminase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tgtctatgtcagcaggatgatcactgcgatggtgaactctaacggtgacaggggtgtgct 692
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Paralichthys
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Pred. No. 37;
0; Mismatches
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                                                                                                                                                                                                              gene
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olivaceus;
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Oncorhynchus k
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Sequence 2148

BP; 578 A; 496 C; 610 G;

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transglutaminase

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Matches 44
                                                                                                                                                                                                                            14-JAN-1992;
27-JUL-1992;
08-DEC-1992;
                   Transglutaminase is used in the prodn. of gelatinous food prods., cosmetics and chemicals. The DNA fragment enables the mass prodr of transglutaminase which is cheap and efficient.
                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                          CDS
                                                            The difference in the 1882 th
                                                                                                                and chemicals
                                                                                                                       New gene encoding trans:glutaminase prodn. of trans:glutaminase for use
                                                                                                                                                        P-PSDB; AAR39519
                                                                                                                                                                  WPI; 1993-259983/33.
                                                                                                                                                                                      Matsui
                                                                                                                                                                                                                                                                    14-JAN-1993;
                                                                                                                                                                                                                                                                                                           EP555649-A.
                                                                                                                                                                                                                                                                                                                                                                      Paralichthys olivaceus.
                                                                                                                                                                                                                                                                                                                                                                                                   Transglutaminase; TGase; fish; Pagrus major; Alaska pollack; Theragra chalcogramma; Paralichthys olivaceus; paste; kamabo
                                                                                                                                                                                                                                                                                                                                                                                                                                 Transglutaminase (fish liver)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ46026 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolated from Pagrus major, Theragra chalcogramma, Paralichthys olivaceus or Oncorhynchus keta. Fish-originated TG's are economical to produce in large quantities.
                                                                                                                                                                                                         (AJIN ) AJINOMOTO KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact 67
                                                                                                                                                                                     Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                           Page 42-44; 85pp;
                                                                                                                                                                                     Motoki M,
                                                                                                                                                                                                                                                                                                                                                                                           food; cosmetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                           92JP-0005166.
92JP-0199803.
92JP-0328010.
                                                           between the sequences of AAQ46025 and AAQ54878 resides base. The change does not alter the translated
                                                                                                                                                                                                                                                                    93EP-0100488
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 26..2092
                                                                                                                                                                                                                                                                                                                              /*tag=
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                                                                                                                                                                                     Nagase
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                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                           SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 24.8; upper pred. No. 37; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (T1882)
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                                                                                                                                                                                      Nakanishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2148
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                                                                                                                        om fish - for the gelatinous food,
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                                                                                                                          cosmetics
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RESULT 34
AAO54878
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AAO 548
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AC AAQ548
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                                                                                                                                                                                         Transglutaminase is used in the prodn. of gelatinous food procosmetics and chemicals. The DNA fragment enables the mass of transglutaminase which is cheap and efficient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transglutaminase; TGase; fish; Pagrus major; Alaska pollack; Theragra chalcogramma; Paralichthys olivaceus; paste; kamaboko; gelatinous food; cosmetic; ss.
                                                                                                                                                             Sequence 2148 BP; 578 A; 496 C; 611 G; 463 T; 0 other;
                                                                                                                                                                                                                                                                  The difference between the sequences of AAQ46025 and AAQ54878 resides in the 1882 th base. The change does not alter the translated
                                                                                                                                                                                                                                                                                                                      Claim 1; Page 45-47; 85pp; English.
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27-JUL-1992;
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tgtctatgtcagcaggatgatcactgcgatggtgaactctaacggtgacaggggtgtgct 720
                    tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact
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                                                                        44;
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                                                                       Conservative
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92JP-0199803.
92JP-0328010.
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26..2092
/*tag= a
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                                                                                      20.2%;
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                                                                                      Score 24.8;
Pred. No. 38;
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                                                                                                                                                                                                                                                                                                                                                                           from fish - for the in gelatinous food,
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                                                                                                        DB 14;
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31-MAY-1996
                                                                 AAQ80534 standard; cDNA to mRNA; 2148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transglutaminase; fish; recombinant production; Pagrus major; Theragra chalcogramma; Paralichthys olivaceus; Oncorhynchus keta;
                                 AAQ80534;
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2148 BP; 578 A; 496 C; 611 G; 463 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 54-56; 94pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                               to produce in large quantities.
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721 gactggtcagtggcac 736
                                                                                                                                                                                                                                661 tgtctatgtcagcaggatgatcactgcgatggtgaactctaacggtgacaggggtgtgct 720
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(first entry)
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Best Local
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                                                                    Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
            WO200055198-A1
                                    Homo
                                                          neurological
                                                                                                                                  Human secreted
                                                                                                                                                         30-JAN-2001
                                                                                                                                                                                 AAC59911;
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Theragra chalcogramma;
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cal disease;
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                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                          578 A; 496 C;
                                                                                                                                                                                                        cDNA; 452
                                                                                                                                                                                                                                                                                                                                                                          20.2%;
                                                                                                                                                                                                                                                                                         83
                                                          infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 മ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; recombinant
Paralichthys
                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                         Score 24.8;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                          610
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                          human;
                                                                                                                                                                                                                                                                                                                                                                                                                          G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production; Pagrus major;
olivaceus; Oncorhynchus keta;
                                                                                                                                  #
5
                                                                                                                                                                                                                                                                                                                                                                                                                         464 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene.
                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        can be produced in large
                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                          other,
                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                     Length 2148;
                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which
                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT 3
AAF26556.
ID AAF2
XX AAF2
XX AAF2
XX DT 27-W
XX DNA
XX Seci
KW Seci
KW autc
KW hype
XX Homc
XX W02(
PN W02(
PF 01-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc conditions, e.g. by protein or gene therapy. The genes and cc conditions, e.g. by protein or gene therapy. The genes are isolated cc from a range of human tissues disclosed in the specification. The cc incleic acids, proteins, antibodies and (ant)agonists are useful in cc the diagnosis, treatment and prevention of: (a) cancer, e.g. breast cc and ovarian cancer, and other cancers of the adrenal gland, bone, bone cc marrow, breast, gastrointestinal tract, liver, lung, or urogenital; cc (b) immune disorders e.g. Addison's disease, allergies, autoimmune cc haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and ce pilepsy; and (f) infectious diseases such as viral, bacterial, fungal cand parasitic infections
                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                              Secreted protein; gene therapy; vaccine; cancer; leukemia; autoimmune disease; allergy; inflammation; graft rejection hyperproliferation; cardiovascular; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relate to the isolation of genes AAC59907-C59956 50 human secreted proteins AAB28702-B28751. The genes can be us generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion for increasing the stability of the fusion protein as compared to the human protein only. The c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 20
                                                                                   Homo sapiens
                                                                                                                                                                     DNA encoding
                                                                                                                                                                                                   27-MAR-2001
                                                                                                                                                                                                                             AAF26556;
                                                         WO200076531-A1
                                                                                                                                                                                                                                                        AAF26556 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 452 BP; 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 315; 391pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1999;
23-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000
                                                                                                                                                                                                                                                                                                                        209 tcactgttcagtgtcacttgtttggtaacactcaacatcaacgtgtgctaccaaa
                                                                                                                                                                                                                                                                                                                                           67 tgactggtaagtttcacatgtaaggtgatacttatcttcaatttattccacacaa 121
                                                                                                                                                                                                                                                                                   38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-587520/55.
DB; AAB28706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secreted proteins and ne therapy protocols ar
                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                       human secreted
                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US06012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0124093
99US-0166989
                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Komatsoulis
                                                                                                                                                                                                                                                        625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and recombinant nucleic acid based pro
                                                                                                                                                                     protein
                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                Score 24.6; D
Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                 No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                       #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                         128
                                                                                                                                                                                                                                                                                                                                                                                                                DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Τ;
                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                            rejection;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Length 452;
                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful
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01-JUN-2000; 2000WO-US15137

21-DEC-2000

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RESULT 39
AAN71405/c
ID AAN714
XX AAN714
XX AAN714
XX Equen
XX Enzyme
KW Enz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                             New DNA sequences for - with secretion of pr transformed fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. For example, they may be used in gene therapy or in vaccines. Typical of diseases which are potentially treatable are cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 47 human secreted preventing, diagnosing and/or treating edisease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                               07-JUL-1986;
29-AUG-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzyme; fungal expression vector; Aspergillus expression vector; Trichoderma; ds.
      Example; Fig 13; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mucor miehei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of ANS-1 which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN71405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAN71405 standard; DNA; 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 625 BP; 174 A; 144 C; 147 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 448; 525pp; English.
                                                                                                                                                                                                                                                                                                       (GENE-) GENENCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (including leukemia), autoimmune diseases, allergies, inflam
graft rejection, hyperproliferation, cardiovascular diseases
(particularly critical limb ischemia and coronary disease) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            grait rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               involving abnormal angiogenesis, neurodegeneration and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to 26 secreted human proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tcactgttcagtgtcacttgtttggtaacactcaacatcaacgtgtgctaccaaa
                                                                                                                                                                                     1987-095049/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-071148/08
                                                                                                                                                                                                                                             Ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben
                                                                                                                                                                                                                                          Gray GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                           86US-0882224
85US-0771374
                                                                                                                                                                                                                                                                                                                                                                                                                                                     86EP-0306624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0138625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM,
                                                                                      or expressing polypeptide in filamentous prod. from the cells, and new vectors an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCI
                                                                                                                                                                                                                                          Hayenga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               increases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВÞ
                                                                                                                                                                                                                                             ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24.6;
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                             Lawlis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transformation efficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ed polypeptides, useful for e.g. cancers, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation,
                                                                                         and
                                                                                                                 fungi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
RESULT 40
AAH62796/c
ID AAH627
XX White
PN W02001
XX White
PN W02001
XX OB-NOV
XX OB-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                        The invention provides the primary nucleotide sequence of the WSBV genome (AAH62889), predicted transcript sequences (AAH62689-AAH62839) and encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences (AAH62840-63160) suitable for use as primers or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to
control viral gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH62796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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*8888888*&
                                                                Primary nucleotide sequence of the shrimp white spot Bacilliform (WSBV), useful for producing viral polypeptides that can be used screen for agents that are useful for treating WSBV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shrimp white spot
antiviral agent; g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A DNA sequence coding for a heterologous polypeptide which can be expressed in and secreted from filamentous fungi is claimed. Pref the DNA sequence codes for bovine preprochymosin, M. meihei preprocarboxyl protease or A. niger preproglucoamylase. Also new are vectors consisting of the DNA sequence plus an operably-linked signal sequence. The vectors may also include a sequence which
                                  Claim 4; Figure 3; 626pp; English.
                                                                                                                                                                                                                                                                                                                                                                31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                 WO200138351-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shrimp white
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH62796 standard; DNA;
                                                                                                                                                                                                                       (PENY-) PE CORP NY.
(THIR-) THIRD INST OCEANOGRAPHY
(SINO-) SINOGENOMAX CO LTD.
                                                                                                                                                                                                                                                                                            24-NOV-1999;
                                                                                                                                                                                                                                                                                                                             08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1864 BP; 786 A; 210 C; 44 G; 732 T; 92 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 aggtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggc
                                                                                                                                    2001-355877/37.
DB; AAG85016.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spot syndrome
                                                                                                                                                                                      Yang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transformation
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                                                                                                                                                                                                                                                                                                                              2000WO-US28888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spot Bacilliform
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                                                                                                                                                                                                                                                                                            99CN-0124717
                                                                                                                                                                                        Не
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistant shrimp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacilliform virus; WSBV; diagnosis; viral infection; yene expression; antisense construct;
                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.0%;
                                                                                                                                                                                        Pham
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus (WSBV) gene 107.
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genome
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infected cells

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create

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RESULT 4
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XX AAH8
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KW Diff
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Best Local S
Matches 42
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                                                                                                                                                                     suppressor genes. (I), and polypeptides encoded by them, are useful as targets for diagnosis or therapy and in screening to determine the effects of an active compound (potential pharmaceutical) on a cell line, particularly for diagnosis and treatment of tumors, especially by modulating expression of (I) (by gene therapy, antisense RNA or ribozyme methods) or by modulating the amount and/or location of (I)-encoded polypeptides (by administration of the polypeptide or its activator, antibody (optionally as a conjugate) or inhibitor). The method allows identification of many Class II tumour suppressor genes (i.e. genes that are not primary targets for tumour-initiating mutations).

AAH81492-AAH82376 represent the human and rat derived nucleic acid fragments described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids differentially expressed between useful for diagnosis or therapy of tumors and \boldsymbol{f}
                                                                                                                                Sequence 3787 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a nucleic acid (I) with differential expression between tumour and normal cells and which has cytostatic activity. (I) work as modulators of Ras activity by inducing expression of tumour work as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 438-439; 579pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grips
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Differential transcription; human; rat; tumour cell; cytostatic; Ras modulator; Class II tumour suppressor gene; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic viral
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     l Similarity
42; Conserv
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Hellriegel M,
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000DE-1004102
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                                                                                                                             898 A; 1210 C; 1073 G; 606 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   979
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Schmitz A, Sers
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                        Score 24.6;
Pred. No. 54;
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Pred.
     Mismatches
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rs C;
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  29;
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  Indels
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4912..5093
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4878..4927
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5767...
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4854..4903
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/note= "trapped exon"
3654..3793
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    "pDJ84g15"
replace(1920,T)
             complement
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/*tag= 1
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/note= "match:
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pDJ84g15"
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/note= "putative polymorphism, pbJ84g15, G in 255h6" complement (15609..15614) /*tag= at 16174..16451
 complement (16867..16939)
/*tag= aw
/note= "trapped exon"
16867..17013
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/note= "trapped exon"
complement (14197..14400)
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/note= "L1 repeat family"
complement (14607..14860)
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/*tag= ai
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/*1067..11368
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/*tag= am
13800..14074
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/*tag= al
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complement (9636..9685)
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/note= "trapped exon"
complement (9467..9583)
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/*tag= ab
/note= "trapped exon"
9351..9678
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                                         /note= "Alu repeat family"
16509..16559
/*tag= av
                                                                                                                                                replace(15091,G)
                                                                                                                                                          /note= "trapped exon"
14930..14979
/*tag= ar
                                                                                                                                                                                                                                                                                                                                                  /*tag= aj
/note= "Alu repeat family"
/1264..11315
                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (10423..10461)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (8414..8447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (7237..7434)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= u
/note= "trapped exon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lement (8055..8165)
                                                                                                                           A in 52b3
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  밁
                   οy
                                                                                    Query Match
Best Local S
Matches 54
48374 tgaaaaatgacttaaagtataggtcaaatatacatgccatgcgggtgctccaagagatgg 48433
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                                                                                             exon
                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                      exon
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                                                                                                                           repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
         Similarity
                                          Conservative
                                                                                                                                                                                                                       30550..3165

/*tag= bs

30550..30863

/*tag= bt

32483..32488
                                                                                                                                                                             /*tag= bu
32483..32488
/*tag= bv
33639..33870
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21450..21499
/*tag= bj
                                                                                complement (34638..34996)

/*tag= by
/note= "TIGGER2 repeat family"
complement (34879..34941)
/*tag= bz
                                                                                                                                           /*tag= bw
/note= "Alu repeat family"
complement (33782..33867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (17427..17606)

/*tag= az

17647..17696

/*tag= ba
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/*tag= br
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24266..24315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= ax
/note= "trapped exon"
17288..17352
                                                                                                                                                                                                                                                                                                                            /note= "putative polymorphism complement (24244..24293)
                                                                                                                                                                                                                                                                                                                                                            replace(24182..24186)
                                                                                                                                                                                                                                                                                                                                                                                  complement (23288..23293)
                                                                                                                                                                                                                                                                                                                                                                                                    complement (23196..23233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Alu repeat family"
21292..21341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Alu repeat family"
20108..20226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (19541..19683)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (19301..19334)
/*tag= bc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (18367..18416)
/*tag= bb
                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (22392..22441)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replace(20729..20767)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "MER20 repeat family"
19688..19975
                                                                                                                                                                                                                                                                                                 /*tag= bq
                                                   20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         ..22956
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                                        Score 24.6; DB 20;
Pred. No. 1.5e+02;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                       (T)5 in pDJ84g15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TAT13) in 52b3"
                                          Indels
                                                             Length 68940;
                                          0;
                                        Gaps
                                         0,
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repeat\_region

exon

exon

exon

exon

exon exon

..9678

promoter

exon

exon exon

..8695

exon

exon exon exon exon

/\*tag= s 6072..6134

exon

polyA\_site

exon

exon exon

repeat\_region polyA\_site

/\*tag=

exon

repeat\_region

exon

variation promoter exon

promoter

polyA\_site

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CDS		CDS	CDS	RBS	CDS	RBS .		CDS	CDS	RBS	CDS	;	CDS	RBS	CDS	RBS	CDS	RBS	CDS		RBS	Key CDS	Micromonospo	Everninomicin fermentation;	Micromonospoi	20-SEP-2001	AAS08693;	S	ULT 43 08693/c	48434 acaaatt	74 taagttto
/note= "No start codon" complement (121813022)	/*tag= r /product= "EvdK" /partial	/product= "EvdJ" 1202712455	1042411176 /*tag= q	102	t (946 "Evdī		22	/product = "EvdG"  /product = "EvdG"  83429364	7272.8327	/product= "EvgF" 6226.6229	62327275 /*tag= 1	/*tag= 1 /product= "EvdE"	/*tag= h 5300 6235	/product= "EvdD" 41344138	4143.5312 /*tag= g				"Evda"		"EvdA" (1389	Location/Qualifiers complement (1321382)	ra carbonacea var. africana.	antibiotic; bottle-neck gene; ds.	DNA encoding biosynthetic enzymes for	iirst entry)		ndard; DNA; 109519 BP.		gatottattgatoatatttttatacotttaattaca 48476	taagtttcacatgtaaggtgatacttatcttcaatttattcca 116
মুমু	মুমুমু	মুমু	ਸ਼੍ਰਾਸ਼੍ਰਾ	মুমু চ	חַ יִּעַיִּים	দ্দু	म्यु म्यु	سائمانس	যুদ্ধ দ	রুণরুণর বুণরুণ	'মুমু	այաց։	ų ų	দ্ৰু দু	দুদ্	বুন্দ্ৰ দু	ni ni	দৌদৌ দ	ם הם הם ה	י פרי ו	יי ביי ביי	لتباشرا	اتا اتا	দ্ম দাদ	ئىر ئىر	ئراتدا	נה נהו	י בי נדי	মৃদ্দা	י עו עי	
r cds				r CDS	T RBS	r CDS	T RBS			T CDS	T RBS	r cds	r rbs	•		T CDS	T RBS	T CDS	T RBS					T CDS			T CDS	T CDS			T RBS
/product= complement /*tag= at	complement /*tag= as /product=	/*tag= ar /product=			/produc complem		complement /*tag= an			/*tag= complem	/product	compleme /*tag=	2667226			<b>,</b> 2, ~	.0 \	compleme /*tag=		/*tag= a	/*tag= 22748	,	N.	\ <b>!</b> \	<b>√</b> 0	•	/product	compleme /*tag=	/product compleme /*tag=	compleme /*taq=	/product compleme
	/note= "No start codon" FT CDS complement (1210813022) FT	/"Lag" r /product= "EvdK"  /product= "EvdK"  /partial FT  /note= "No start codon"  CDS complement (1210813022)  FT	/product= "EvdJ" FT 1202712455  /*tag= r /product= "EvdK" FT CDS /product= "EvdK" FT /partial FT /note= "No start codon" FT /CDS complement (1210813022) FT	CDS 1042411176 FT	RBS (complement (1023210235) FT CDS (**Lag= p FT CDS 104241176 FT CDS /**tag= q FT CDS /**tag= q FT CDS /**product= "EvdJ" FT CDS 1202712455 FT CDS /**product= "EvdK" FT CDS /**product= "EvdK" FT CDS /**product= "EvdK" FT CDS /**product= "No start codon" FT CDS complement (1210813022) FT CDS	CDS complement (946310224)  /*tag= o	RBS 833.8336 FT CDS /*tag= n FT CDS complement (9463.10224) FT CDS complement (10232.10235) FT RBS complement (10232.10235) FT CDS /*tag= p FT CDS /*tag= q FT CDS //product= "EvdJ" FT CDS //product= "EvdJ" FT CDS //product= "EvdJ" FT CDS //product= "EvdJ" FT CDS //product= "EvdK" FT CDS //product= "EvdK" FT CDS //product= "EvdK" FT CDS //product= "No Start Codon" FT CDS //partial //p	/*tag= m	/product= "EvdG"	CDS	RBS 626622 EVGFT  /*tag= ak /*tag= k  7728327  /*tag= ak /*tag= k  7728327  /*tag= ak /*ta	CDS	/*tsg-11 /product= "BydE" 6232.7275 6232.7275 RBS	#tag= h  /*tag= 1  /*tag= 1  /*tag= 1  /*tag= 1  /*tag= 1  /*product= "EvdE"  CDS	/product= "EvdB"  /*tag= 1	CDS	RBS complement (3867.3870)  RBS (143.5312  (150.512)  RBS (143.138  (150.535	CDS	RBS  /*tage to CDS  /	RBS / Cappionent (14900011)  RBS / Cappionent (2618.2622)  RBS / Cappionent (2618.2622)  CDS / Cappionent (2622.3660)  / CDS / Cappionent (2622.3660)  / CDS / Cappionent (2667.3870)  RBS / Cappionent (2667.3870)  CDS / Cappionent (2667.3870)  C	CDS	RBS	Key Concation/Qualifiers Complement (1321382)  RBS	Micromonospora carbonacea var. africana.  Rey	Evernitacicit; abtilotic; bottle-neck gene; orthomicin;   Evernitacion;   dx.	### Altromonospota DAM elmocling Docsynthatic enzymes for Portninomycin.  ###################################	### Accomplement (1231-1362)  ### Accomplement (1231-1362)  ### Complement (1231-1362)	ASO8953;  Micromonopora Obh encoding biosynthetic enzymes for Everninomycin.  Persilomnicin; antibiotic; bothle-neck gene; orthonicin;  Everninomicin;  Everni	standard; DMA; 109519 BP.  27 CDS  28 (1first entry)  28 (25 continue)  29 (25 continue)  29 (25 continue)  20 (25 conti	SULPAY   A   SUL	### CDS   COMPANDED   PROCESS   PROC

hypertension

AIDS;

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             δÃ
                                                         Matches
                                   Query Match
Best Local
76022 AGATGGGGTACGACTCGGACGACCCGATCGCCCACGGCGAGGTCGGCAAGGTCGG 75968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RBS
        18 agatgeettacaaccetgatgacctaatggegcaatgegagggetgeactgactg
                            36;
                                   Similarity
                            Conservative
                                                                                                                                                                                                                    51627..52715
/*tag= bi
/product= "EvsB"
                                                      /*tag= bq
/product= "EvbC2"
56961..58709
                                                                              complement
                                                                                           complement (56100..56103)
                                                                                                                complement
                                                                                                                              complement (55125..55128)
                                                                                                                                                   complement (54362..55117)
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53554..54207
                                                                                                                                                                                       52889..53557
/*tag= bk
                                                                                                                                                                                                                                                      complement (47156..49234)
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                                                                                                                                                                                                                                                                                           complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (40887..41576)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product=
                                                                                                                                       /product= "EvbB"
                                                                                                                                                             /product= "EvbA"
                                                                                                                                                                                                                                                                                                                   /product= "EvrY"
                                                                                                                                                                                                                                                                                                                                        /product= "EvrX"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "EvrU"
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                                                                                                   'product= "EvbC"
                                                                                                                         *tag=
                                                                                                                                                                    '*tag=
                                                                                                                                                                                                                                           product= "EvsA"
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                                                                                                                                                                                                                                                                               'product= "Evr2"
                                                                                                                                                                                                                                                                                                                                                                             product=
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                                                                                                                                                                                                                                                                                                                                                                                                                "EVYV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Evrs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (40216..40890)
                          Pred. No. 1.7e.
0; Mismatches
                                                                                                                (55135)
                                                                                                                                                                                                                                                                                            (45962..46714)
                                                                                                                                                                                                                                                                                                                                                     (43799..44866)
                                                                                                                                                                                                                                                                                                                                                                                         (42810..43799)
                                                                             (56184..56813)
                                                                                                                 . 56094)
                          1.7e+02;
hes 19;
                                         DВ
                                         Length 109519;
                           Indels
                           0;
             72
                           Gaps
                           0;
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RESULT

Sequence coagulation;

294 BP;

96 A; 51 c;

8

G; 79 7

0 other;

a contraceptive

6

inhibit thrombosis;

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AAC75339/c
ID AAC75339 standard; cDNA; 294
                                                        antiinflammatory; antibacterial; antivital; antifungal; antirheumatic; antiinflammatory; antibacterial; antivital; antifungal; antirheumatic; antiinfyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1999;
02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                      AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hyperten neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AI cholesterol ester storage; systemic lupus erythematosus; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; open reading frame; OREX; detection; cytostatic; hepatotropic; vulnerary; antipscriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                             immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
antidiabetic; hypotensive; dermatological; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 1399; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-602362/57.
P-PSDB; AAB41130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORFX ORF894 polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2000;
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99US-0127728
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frame

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RESULT 45
AAA01147/c
ID AAA01147 standard; cDNA; 300 BP.
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Best Local (
                                                                                                                                                                                                                                                                                          Williams LT, Esc.
Reinhard C, Glese K, ka
Reson G, Drmanac R, C;
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       sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                                  AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test
                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                        (CHIR )
(HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probe; detection; cancerous state; metastasis; identification;
breast cancer; oestrogen receptor-positive breast cancer; therapy;
oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                     cells
                                                                                                                                                                                                                                               Polynucleotide library used to determine cancerous states of mammalian
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98US-0085537.
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Randazzo F, Kennedy GC, I
Crkvenjakov R, Dickson M,
Garcia V, Jones LW, Stav
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Pred. No. 27;
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responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-negative breast cancer, lung cancer, and colon cancer.
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Sequence 300 BP; 85 A; 72 C; 73 G; 70 T; 0 other;

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Search completed: March 19, Job time: 2850 sec 2002, 10:21:41

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aatgcgaggg 	2; Length 54; Indels	Region	
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US-08-477-451-25

J. Sequence 25, Application US/08477451

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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: Helicobacter Pylori Cagi Region
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CORRESPONDENCE ADDRESS:
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                                                                                     CORRESPONDENCE ADDRESS
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                         NUMBER OF SEQUENCES:
                              STREET: 4500
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CITY: Emeryville
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                 COUNTRY:
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REGISTRATION NUMBER: 33,113
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Pred. No. 5.5;
0; Mismatches
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; TOPOLOGY: 1;; MOLECULE TYPE: US-08-477-451-25
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                 REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8145 CGTTAAATTCCCCCTGTTAATTTGCTAATATTTAAGATATTGTTCCCCCACAGC 8196
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIBULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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STREET:
CITY: Sa
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TELEPHONE:
                                                  REGISTRATION NUMBER: 38,498
                                                                                                                              APPLICATION NUMBER: FILING DATE: 17-FEE
                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 510-601-2708
TELEFAX: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: McClung, Barbara (REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                 California
                                                                                                                                                                                                                                                                                                                                                            Floor
                                                                                                                                                                                                                                                                                                                                                                         E: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Street Tower, 20th
                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
   415/543/9600
                                                                                                                              17-FEB-1995
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Pred. No. 8.9;
                                      L5371A-17
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SEQUENCE CHARACTERISTICS

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; NAME/KEY:
; LOCATION:
US-08-741-134-1
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   Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08741134 Patent No. 5861498
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Best Local Similarity
Matches 36; Conserv
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                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                        FEATURE:
                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,163
FILING DATE: 01-NOV-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5990 GACATGGCTTTCAACGCCGATGTCGGTATGGCGACCTGCAAACGCTGTGGTGAC 6043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.11
                                                                                                                                                  TOPOLOGY:
                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJI
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                NAME: DeLuca, Mark
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                                                                                                                                                                                          2255 base pairs
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    Conservative
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                                                                                        160..1398
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                                                                                                                                                                double
                                                                                                                                                  relevant
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                20.3%;
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Emad S.
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Score 25; DB Pred. No. 6.5; 0; Mismatches
   0;
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Pred. No. 10;
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                DB
5.5;
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                             Length 2255;
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US-08-164-839-30
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 Matches
               Query Match
Best Local (
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                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/0
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1695 TAGACAACAATGTGGTATACCTGCAATATTTTACTGATGTTCAAT 1651
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                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                             LENGTH: 2064 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                     NAME: Oblon, No. 5514573man REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: OBLON, SPIVAK, McCLELLAND, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway,
                                                                                                                                       TISSUE TYPE:
                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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               Similarity
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(703)413-2220
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                                                                                                                                                  Paralichthys olivaceus
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                                                                                                                                       liver
                                                                                                                                                                                  cDNA to mRNA
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, HIROSHI
: GENE ENCODING TRANSGLUTAMINASE DERIVED
               20.2%;
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Score 24.8; D
Pred. No. 7.4;
0; Mismatches
0;
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                            DB 1;
32;
                            Length 2064;
Indels
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0,
Gaps
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US-08-164-839-32
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US-08-164-839-32
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: YASUED
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APPLICANT:
APPLICANT:
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ORIGINAL SOURCE:
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APPLICATION NUMBER: 08/01
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                 633
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68 gactggtaagtttcac 83
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                                                                                                         Local
                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Virginia
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                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact 67
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                              TGTCTATGTCAGCAGGATGATCACTGCGATGGTGAACTCTAACGGTGACAGGGGTGTGCT 692
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5. 5514573
                                                                                                                                                                                                                                                                                                                       H: 2064 base pairs nucleic acid
                                                                                                         Similarity
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(703)413-2220
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                                                                                          Conservative
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                                                                                                         20.2%;
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                                                                                      Score 24.8; DB 1;
Pred. No. 7.4;
0; Mismatches 32,
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US-08-583-799-30
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APPLICANT: YASUED
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 08/0
FILING DATE: 14-JAN-1993
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                               Local
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GACTGGTCAGTGGCAC
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                         gactggtaagtttcac 83
                                                         TGTCTATGTCAGCAGGATGATCACTGCGATGGTGAACTCTAACGGTGACAGGGGTGTGCT 692
                                                                                                                               Similarity
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Y: U.S.A.
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(703)413-2220
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                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                     double
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                                                                                                               Score 24.8; DB Pred. No. 7.4; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-599-0
                                                                                                                                             DB 1;
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US-08-583-799-32
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US-08-583-799-32
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Sequence 32, App-
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ORIGINAL SOURCE:
ORGANISM: Para
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,799
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/0 FILING DATE: 14-JAN-1993 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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STATE: Virginia
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                                                                                                                                                                                    Similarity
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1755 Jefferson Davis Highway, Fourth Floor
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); Mismatches
                                                                                                                                                                                 Score 24.8;
Pred. No. 7
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US-08-164-839-71

US-08-164-839-71

; Sequence 71, Application US/08164839

; Patent No. 5514573

; GENERAL INFORMATION:
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Best Local Similarity
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
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NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
FILING DATE: 14-JAN-1993
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                                                                                                         721 GACTGGTCAGTGGCAC 736
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COUNTRY: U...
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LOCATION:
                                                                                                                                    68 gactggtaagtttcac 83
                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Virginia
                                                                                                                                                                                    8 tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact 67
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                 POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid

    P.C.
    1755 Jefferson Davis Highway, Fourth Floor

                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703)413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAKANISHI,
                                                                                                                                                                                                                                                                                                                     CDS
26..2092
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                                                                                                                                                                                                                                                                                                                                                                                Paralichthys olivaceus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                               cDNA to mRNA
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                                                                                                                                                                                                                                           20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM FISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HISASHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08/004,729
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                                                                                                                                                                                                                           Score 24.8; DB Pred. No. 7.6; 0; Mismatches
                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                             32;
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US-08-164-839-71
                                                                                       US-08-583-799-69
                                                                                                      RESULT
                                          Patent No. 5607849
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      Matches
                                                                         Sequence 69,
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/004,729

FILING DATE: 14-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: ODLON, NO. 5514573man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-599-
             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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APPLICANT:
                                                                                                                                                                                                             661
                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)412-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                 721
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                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                 GACTGGTCAGTGGCAC 736
                                                                                                                                                                             gactggtaagtttcac 83
                                                                                                                                                                                                          TGTCTATGTCAGCAGGATGATCACTGCGATGGTGAACTCTAACGGTGACAGGGGTGTGCT 720
                                                                                                                                                                                                                                      tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact 67
                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                    Similarity 57.9
44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 2148 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virginia
                                                                        Application US/08583799
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1755 Jefferson Davis Highway, Fourth Floor
MOTOKI, MASAO
                           YASUEDA, HISASHI
                                                                                                                                                                                                                                                                                                                                                          CDS
26..2092
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               NAKANISHI,
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                    20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/164,839
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                                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                      RESULT
                                                                                                         Sequence 71, Application US/08583799 Patent No. 5607849
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                              GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: FEATURE:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Oblon, No. 5607849man F.
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
FITLE OF INVENTION:
                 APPLICANT:
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                               PPLICANT:
                                                                                                                                                                                                      721 GACTGGTCAGTGGCAC 736
                                                                                                                                                                                                                                                                  661 TGTCTATGTCAGCAGGATGATCACTGCGATGGTGAACTCTAACGGTGACAGGGGTGTGCT 720
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1755 Je
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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                                                                                                                                                                                                                         gactggtaagtttcac
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                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
DEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oblon,
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                                            YASUEDA, HISASHI
NAKANISHI, KAZUO
MOTOKI, MASAO
                                                                                                                                                                                                                                                                                                                               Conservative
                 MATSUI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (703)412-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA to mRNA
HIROSHI
GENE ENCODING TRANSGLUTAMINASE DERIVED
                                 KAZUO
                                                                                                                                                                                                                                                                                                                                            20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPIVAK, McCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                      83
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                                                                                                                                                                                                                                                                                                                              Score 24.8; DB Pred. No. 7.6; 0; Mismatches
                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-599-0
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                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                          Length 2148;
                                                                                                                                                                                                                                                                                                                               Indels
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TITLE OF INVENTION:

FROM FISH

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US-09-318-448-5/c
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; LOCATION:
US-08-583-799-71.
                                                                 Sequence 5, Application US/09318448
Patent NO. 6210950
GENERAL INFORMATION:
APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING,
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                 CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
SOFTWARE: PatentIn Ver. 2.0
                  NUMBER OF SEQ ID NOS: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2148 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Oblon, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
PAPELICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                    721 GACTGGTCAGTGGCAC 736
                                                                                                                                                                                                                                                                                                                                                       661 TGTCTATGTCAGCAGGATGATCACTGCGATGGTGAACTCTAACGGTGACAGGGGTGTGCT 720
                                                                                                                                                                                                                                                                                                         68 gactggtaagtttcac 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              8 tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 2148 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (703)413-2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             20.2%;
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Pred. No. 7.
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6
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                                                                                                      PREVENTING, AND TREATING
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RESULT 15
US-08-152-019A-44
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; ORGANISM: Homo sapiens
US-09-318-448-5
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                                                                          US-08-152-019A-44
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LENGTH:
  Matches
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                                                                                                                                                                       TELEX: 910 277299 FHT UR INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: OSMAIN, Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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ADDRESSEE: FLEHR, HOHBACH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NEURAL AXON OUTGROWTH MODULATORS NUMBER OF SEQUENCES: 46
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                                                                                                                                                                                       TELEPHONE: (415) 398-3249
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 12-NOV-1993 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                 Local
                                                                                                   TOPOLOGY:
                                                                                                               STRANDEDNESS:
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                                                                                                                                           LENGTH:
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7720
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                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: 4 Embarcadero Center, Suite 3400 San Francisco
                                                                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                           1839 base pairs
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Kennedy, Timothy
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  Conservative
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Jessell, Thomas
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SYSTEM: PC-DOS/MS-DOS
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              19.7%;
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              Score 24.2;
Pred. No. 12;
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Mismatches
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  48;
  Indels
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RESULT 17
US-08-727-034-5
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                                  Sequence 5, Application US/08727034 Patent No. 5665872 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 343-4342 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION UMBER: 36,627
REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,677
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jessel, Thomas
APPLICANT: Dodd, Jane
TITLE OF INVENTION: Netrins
NUMBER OF SEQUENCE: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1839 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                          176 CTGTTATTGCTAGTGATACATGCGGAACAAACCGACCAGACAAGTATTGTACTGTGAAGG 235
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CALTERDAY: STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALTERDAY:
                                                                                                                                                        236 AGGGTCCGGATGGAATTATCCGTGAGCAATGTGACACTTGT 276
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                                                                                                                                                                                61 ctgcactgactggtaagtttcacatgtaaggtgatacttat 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                               ch 19.7%;
1 Similarity 52.5%;
53; Conservative
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Kennedy, Timothy
Placzek, Marysia
Jessel, Thomas
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SAITO, YASHUSI
IWASAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                YASHUSHI
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Pred. No. 12;
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                                                                                                                                                                                       Sequence 6, Application US/08727034 Patent No. 5665872
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                GENERAL INFORMATION:
APPLICANT: SAITO, YASHUSHI
APPLICANT: MASAKI, AKIO
APPLICANT: ARAI, KOICHI
APPLICANT: YAMAZAKI, HIROY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATE: 08-ULI.

FILING DATE: 08-ULI.

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 261440/1995
                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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APPLICATION NUMBER:
FILING DATE: 24-APR-
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                ADDRESSEE:
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                                                                                                  YAMAZAKI, HIROYUKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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              OBLON, SPIVAK, McCLELLAND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       703-413-3000
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TITLE OF INVENTION: NOVEL LDL RECEPTOR ANALOG TITLE OF INVENTION: THE GENE CODING THEREFOR NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5248 CCACCAGATATCCACATTGACAGCTATGGTGAAAATTATCT 5288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 gcactgactggtaagtttcacatgtaaggtgatacttatct 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
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MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 6642;
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                                                                                                                    PROTEIN AND
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                                                                 Sequence 2, Application US/08253785 Patent No. 5633363
                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                 5328 CCACCAGATATCCACATTGACAGCTATGGTGAAAATTATCT 5368
                                                                                                                                                                                                                               5268 GGAATAGGAAACTGGAGCGATTCTAAAATCCATTACCACCATAAAAGGAAAAGTGATCCCA 5327
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 261440/1995
FILING DATE: 09-OCT-1995
                  APPLICANT:
                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                         Local
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LOCATION: 165..6722
OTHER INFORMATION: /fun
OTHER INFORMATION: encc
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LOCATION:
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OPERATING SYSTEM: F
SOFTWARE: PatentIn
                                                                                                                                                                                            63 gcactgactggtaagtttcacatgtaaggtgatacttatct 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: sig_peptide LOCATION: 81..164
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                                                                                                                                                                                                                                                                                             l Similarity
53; Conserv
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81..6725
Colbert, James T. Held, Bruce M. Wurtele, Eve S.
                                                                                                                                                                                                                                                                                             Conservative
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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24-APR-1996
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                                                                                                                                                                                                                                                                                                             19.7%; 52.5%;
                                                                                                                                                                                                                                                                                                                                                                                          encode the mature peptide"
/note= "Identification Method: S"
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Pred. No. 19;
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                                                                               COUNTRY:
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US-08-975-316-53/c
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Best Local Similarity
Matches 44; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
                                                                                                                                                                                                                             APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1001 TAAATCTTCCATGCCTTGGAACCCATATGACATTGTGGCCTTATTTGATTCATACTCACC 942
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TELECOMMUNICATION INFORMATION:
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NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                   COMPUTER READABLE FORM:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                  COMPUTER:
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LOCATION: 51..1850
OTHER INFORMATION:
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STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                 MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                       Seattle
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                  IBM Compatible SYSTEM: DOS
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FastSEQ for Windows Version 2.0
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                                                     Diskette
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56.4%;
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Pred. No. 21;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316

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TELEFAX: 206-20
INFORMATION FOR SEQ
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APPLICANT:
                                       ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
                                                                                                                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Grierson, Alastair
TITLE OF INVENTION: MATERIALS AND METHODS FOR THE
TITLE OF INVENTION: MODIFICATION OF PLANT LIGHIN (
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467
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                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pair-
                                                                                                                                                                                                                                                                               STREET: 2501 r
                                                                                                               CLASSIFICATION:
                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                       STATE:
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                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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              206-269-0563
                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
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                             206-269-0565
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01 Elliott Avenue, Suite 4185
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BER: 11000/1003C1
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Pred. No. 15;
0; Mismatches
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TGATGTCCATGGCTAGAATCTTTCCATCATCGGGCAATGCAAGGGCTGTGCTGAGAAGCG 391

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US-08-975-316-6
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 Matches
                           Query Match
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Matches
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                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/7
FILING DATE: September 1
ATTORNEY/AGENT INFORMATION:
                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1026 base pairs
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, APPLICANT: and GRIERSON, Alastair W. TITLE OF INVENTION: MATERIALS AND METHODS FOR TITLE OF INVENTION: THE MODIFICATION OF PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 AGTAACCAGTGTA 378
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                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
Local Similarity
nes 42; Conserv
                                                                                                                                                                      TELEX:
                                                                                                                                                                                   TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                                                                                                                                                         NAME: SLEATH, Janet REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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ber 11, 1996
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              Score 23.4;
Pred. No. 19;
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Pred. No. 19;
 Mismatches
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390 AGTAACCAGTGTA 378

US-09-211-710-6/c

Sequence 6, Application US/09211710A Patent No. 6204434

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; OTHER INFORMATION: beta-cyclase
US-09-201-641-1
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; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-211-710-6
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Best Local Similarity
Matches 42; Conserv
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                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09201641A Patent No. 6232530
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cunningham Jr, Francis X
APPLICANT: DellaPenna, Dean
TITLE OF INVENTION: Method for Regulating Carotenoid Biosynthesis
TITLE OF INVENTION: Marigolds
FILE REFERENCE: Quest 41-162
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/201,641A CURRENT FILING DATE: 1998-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 11000.1003c3
CURRENT APPLICATION NUMBER: US/09/211,710A
CURRENT FILING DATE: 1998-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka APPLICANT: Grierson, Alastair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Tagetes erecta
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                          LENGTH: 1959
1005 tcaatatgataagccttataaccctgggtaccaagtggc 1043
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                                                                                      Local Similarity
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                                                                    Conservative
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                                                                                    18.7%;
74.4%;
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                                                                                    Score 23; DB 4;
Pred. No. 33;
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Pred. No. 19;
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US-08-244-686-1
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                                                                                        Matches
                                                                                                        Query Match
Best Local :
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                1322 ATTGGGAGATGCGGGGTGCTGCGTACGCTCTAAGGTAGGGCATTTAAAGGGATATTTAGC 1381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: intron
LOCATION: 581..629
LDENTIFICATION METHOD:
OTHER INFORMATION: /evi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                 43 aatggcgcaatgcgagggctgcactgactggtaagtttcacatgtaaggtgatacttatc 102
                                                                                                                                                                                                              OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
                                                                                       Local Similarity 55.7 les 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: PAW14B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                          LOCATION: join(351..580, 630..1035)
IDENTIFICATION METHOD: experimental
                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
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ttcaatttattccacacaa 121
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SYSTEM: PC-DOS/MS-DOS
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join(432..5
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                                                                                                       18.7%;
55.7%;
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                                                                                                                                                                                                                                                                                                                     DD: experimental
/EC_number= 3.2.1.8
/product= "endoxylanase
/evidence= EXPERIMENTAL
                                                                                                                                                                                            D: experimental.
FEC_number= 3.2.1.8
/product= "pre-pro endoxylanase
/evidence= EXPERIMENTAL
                                                                                                                                                                                /gene= "exlA"
                                                                                                                                                                                                                                                                                                       /gene= "exlA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=
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/evidence= EXPER
                                                                                                                                                                                                                                                                                                                                                                                 .580, 630..1032;
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                                                                                        Score 23; DB Pred. No. 34; 0; Mismatches
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                                                                                                                      DB
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                                                                                                                     Length 2059;
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RESULT 27
US-08-852-091-7/c
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US-08-369-796-7
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US-08-369-796-7/c
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                       Sequence 7, Application US/08852091 Patent No. 5883228
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Best Local Similarity
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GENERAL
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SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pair:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ORGANISM: Mou
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION:
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EDNESS: both
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Pred. No.
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US-08-820-754-7/c
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NAME/KEY:
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TITLE
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Sequence 7, Application US/08820754 Patent No. 5976835
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Best Local Similarity
                                                                               GENERAL INFORMATION: APPLICANT: Darnel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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PRIOR APPLICATION DATA:
08/369,796
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LENGTH: 2277 base pairs
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
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   CLONE: Murine Stat91
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OPERATING SYSTEM: PC-DOS/MS-DOS
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New Jersey
INVENTION:
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                                                           Darnell Jr., James E. Schindler, Christian W.
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Curt M. Ho
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                                Wen, Zilong
                                                 Fu, Xian-Yuan
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68.1%;
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 RECEPTOR RECOGNITION FACTORS, PROTEIN
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Pred. No.
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US-08-956-652-7/c

; Sequence 7, Application US/08956652

; Patent No. 6013475
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GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
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LENGTH: 2277 base pairs
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
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PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/854,296
FILING DATE: 19-MAR-1992
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APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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TELEPHONE: 201 487-5800
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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STATE: New Jersey
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ER: 600-1-073 CIP
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Pred. No.
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Mismatches
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US-08-956-652-7
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INFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy
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NUMBER OF SEQUENCES:
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                                                                              Local
                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
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411 Hackensack Avenue
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                                                                                                                                                                                                                                                                                    NO
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UMBER: US_07/980,498
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68.1%;
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                                                            Score 23; DB 3; Length 2277; Pred. No. 35; o; Mismatches 15; Indels
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RESULT 30
US-08-956-869-7/c
Geauence 7, Appl
                                                                                          ; NAME/KEY:
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US-08-956-869-7
Query Match
Best Local Similarity
Thehes 32; Conserva
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                      ORIGINAL SOURCE:
ORGANISM: Mouse
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELECHONE: 201 487-5800
                                                                                                                                         FEATURE:
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                        CLONE:
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TOPOLOGY: unl
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
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                                                                                                                                                                                                                                                                                                         ENGTH: 2277 base pairs
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Fu, Xian-Yuan
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                                                                                                                                                                                                                                                               unknown
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68.1%;
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Pred. No.
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LOCATION:
US-08-948-547-7
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                              FEATURE:
NAME/KEY:
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MEDIUM TYPE: Floppy disk
                                                          IMMEDIATE SOURCE:
   CLONE: Murine Stat91
                                                                                                       ORIGINAL SOURCE:
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APPLICATION NUMBER: WO U
FILING DATE: 19-MAR-1993
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PRIOR APPLICATION NUMBER: US 07/854,296
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ADDRESSEE: Klauber & Jackson
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                                                                                          ORGANISM:
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                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., REGISTRATION NUMBER:
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FILING DATE: 11-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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EDNESS: both
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24-SEP-1993
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Best Local Similarity
Matches 32; Conserv
                Query Match
Best Local Similarity
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      Matches
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                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REGESTRATION NUMBER: 600 TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
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APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
                                                                                                                           FEATURE:
                                                                                                                                                      ORGANISM: Mous
IMMEDIATE SOURCE:
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ANTI-SENSE: 1
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APPLICATION NUMBER: PC
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.25
                                                                                           NAME/KEY:
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    Conservative
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 Score 23; DB 5;
Pred. No. 35;
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Best Local Similarity
Matches 47; Conserva
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-27
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US-09-318-448-30
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APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Applica Patent No. 6287569 GENERAL INFORMATION:
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Sequence 30, Appiro
-+ No. 6210950
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                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KIPPS, TH
APPLICANT: WU, YUNQI
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                                  2910 ttgaaaatgactgctaccttatatcccttctcaccttaggcctctcttctgtggaaactc 2969
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                                                                                                        Local Similarity 60.
nes 38; Conservative
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                                                     7 ttgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcac
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Pred. No. 45;
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Pred. No. 41;
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US-07-792-600-1/c
                                                                       SEQ ID NO 1
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local :
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                                                                                     SOFTWARE:
                                                                                                      EARLIER APPLICATION NUMBER: 07/792,600 EARLIER FILING DATE: 1991-11-15 NUMBER OF SEQ ID NOS: 35
                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/157,021A CURRENT FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        APPLICANT: Copeland, William C. APPLICANT: Wang, Teresa S. F. TITLE OF INVENTION: Drug Design Assay FILE REFERENCE: STDU-03484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: STDU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
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            LENGTH: 4440
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 68.1%; es 32; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 199111 CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC STRANDEDNESS:
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                                                                                     PatentIn Ver. 2.0
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 5433
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-157-021-35
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                                                        Query Match
Best Local Similarity
Matches 32; Conserv
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Best Local Similarity
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APPLICANT: Wang, Teresa S. F.
TITLE OF INVENTION: Drug Design Assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/157,021A CURRENT FILING DATE: 1998-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Copeland, William C.
APPLICANT: Wang, Teresa S. F.
TITLE OF INVENTION: Drug Screen
FILE REFERENCE: STDU-03485
                                                                                                                                                                                                                                                                                                             FILE REFERENCE: STDU-03484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
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NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 4440
408 GGTTTTGTCACTGCGAGCTTCTTTACATTCCTCTTGTCTTTATTGCG 362
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Similarity 68.1%;
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                                                        Score 23; DB Pred. No. 49; 0; Mismatches
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; ORGANISM: Homo sapiens
US-09-156-842-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-483-503A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-156-842-35/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 35, Application US/09156842A Patent No. 6103473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --yuence 2, Application US/08483503A
Patent No. 6017880
GENERAL INFORMATTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1991-11-15
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Copeland, William C. APPLICANT: Wang, Teresa S. F. TITLE OF INVENTION: Drug Screening FILE REFERENCE: STDU-03485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                     APPLICATION NUMBER: US
FILING DATE: 07-JUN-19
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 5433
                                                                                                                         APPLICATION NUMBER: US 08/209,040
EILING DATE: 09-WAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,369
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dripps, David J.
TITLE OF INVENTION: INHIBIT
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wahl, Sharon M.
                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Eisenberg, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408 GGTTTTGTCACTGCGAGCTTCTTTACATTCCTCTTGTCTTTATTGCG 362
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
COMPUTER: IE
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
                                 TELEPHONE:
                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                            NAME: Barker, M. Paul
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      w
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                   202-408-4400
                                 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                07-JUN-1995
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68.1%;
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US-08-896-605A-7/c
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GENERAL INFORMATION:
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                                                                                                                                                                               TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1:
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patent In Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 180 base pairs
TYPE: nucleic acid
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 18 July PRIOR APPLICATION DATA:
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MOLECULE TYPE:
                                                                                   FEATURE:
                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CGTGACTTGAAGTGTTGCATGGGCATGTGTGGGAAATCCTGCGTTT 166
                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                   NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 19-JU
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08 FILING DATE: 18 July 1997
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              NAME/KEY:
                                                                                                               TOPOLOGY:
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                                                                    NAME/KEY:
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                                         IDENTIFICATION METHOD:
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DENTIFICATION METHOD:
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419 Seventh Street, N.W., Suite 300
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                                                         leader peptide 1..108
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                                                                                                cDNA to mRNA
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                peptide
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Pred. No. 16;
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Best Local
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INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TATELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 2: FILING DATE: 25-JUL-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP 213,267/1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                      TELEPHONE: 202-737-3528
    Local Similarity 50.0 ies 57; Conservative
                                                                                                  IDENTIFICATION METHOD: NAME/KEY: mat peptide LOCATION: 109..579
                                                                                                                                                                                                                                                                                                                                       NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 1
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                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 31,474/1997 FILING DATE: 31-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
                                                                                                                                            LOCATION:
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                                                                                                                                                        NAME/KEY:
                                                                                    [DENTIFICATION METHOD:
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5. 5891663
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419 Seventh Street, N.W., Suite 300
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SYSTEM: PC-DOS/MS-DOS
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              18.5%;
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Score 22.8; D
Pred. No. 25;
0; Mismatches
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Pred. No. 2
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                            DB 2;
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  57;
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  APPLICANT:
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; FEATURE:

NAME/KEY: misc_feature

; LOCATION: (1)...(680)

; OTHER INFORMATION: n = A,T,C

US-09-328-111-774
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                                                                                                                                                                    Sequence 81, Application US/08943731
Patent No. 6265157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 774
LENGTH: 680
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Best Local :
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                                                                                                              GENERAL INFORMATION:
APPLICANT: PROCKO
APPLICANT: SPOTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: US 60/088,801 EARLIER FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Burgess, Christopher C. APPLICANT: Bushnell, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Catino, Theodore J
APPLICANT: Derti, Adnan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ford, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Carroll III, Eddie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                         APPLICANT:
                                                                             APPLICANT:
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                                       APPLICANT
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51; Conservative
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COLIGE, ALAIN EARLY, JAMES
                                                                           SEREDA,
                                                                                                                SPOTILA,
                                     PACK, MICHAEL
                                                                                            DELTAS,
                                                         LARSON, ANDREA W.
                                                                                                                                  PROCKOP, DARWIN J.
                                                                                              CONSTANTINOS
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Pred. No. 27;
0; Mismatches
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                                                                                                                                                                                                                                                           Sequence 2, Application US/08884324 Patent No. 6060283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph. D., KATHRYN
ORGA-27
                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 911 base pairs
TYPE: nucleic acid
                                                                                                                                                                                 APPLICANT: Takanori OKURA
APPLICANT: Kakuji TORIGOE
APPLICANT: Masahi KURIMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ANDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
                                                                                                                                               TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/943,731
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MEDIUM TYPE: Floppy disk
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                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                         774 CACTAGCTGGGAAGTGTGAAAAGAGTTCTGAAATTTTTCTTCTATTTTT 725
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CITY: PHILADELPHIA
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                                    STATE: D.C
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               COUNTRY:
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Pred. No. 30;
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                                                                         Suite 300
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Search completed: March 19, 2002, 09:58:41 Job time: 1615 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION UDBER: JP 185,305/96
FILLING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                337
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                                                                        277 CCAGGTTTTCATCATCTTCAGCTATAAAGTAAAGCGTATTGTCAATAAATTTCA 224
                                                                                                                                                                                       Local Similarity hes 57; Conserv
                                                                                        63 gcactgactggtaagtttcacatgtaaggtgatacttatcttcaatttattcca 116
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TISSUE TYPE:
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                                                                                                                                                                                                                                                                                                         NAME/KEY:
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LOCATION: 286.
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202-737-3528
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Pred. No. 32;
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pir2:T38660
pir1:X48729
pir2:H7267
pir2:H7267
pir2:T42756
pir2:T32633
pir2:A31788
pir2:A31788
pir2:B66073
pir2:B66073
pir2:H70109
pir2:H70109
pir2:H70109
pir2:T16487
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pir2:T41449
pir2:T21433
pir2:T21430
pir2:T21430
pir2:T03455
pir2:T03454
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pir2:T03454
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pir2:H85462
pir2:S69047
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Database length: 76174552
Search time (sec): 37.240000
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Database: PIR_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search information block:
Query: US-09-684-016-48411
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  GenCore software,
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in 5-oxoprolinase (ATP-hydrolyzin in hypothetical protein Y47H90.2 in hypothetical protein F15E6.1 is in hypothetical protein sugarcane bacilli polyprotein - sugarcane bacilli polyprotein - sugarcane bacilli polyprotein - sugarcane bacilli polyprotein - sugarcane dinucleot molybdopterin-guanine dinucleot ABC transporter, ATP-binding printer protein SPCC645.13 ippothetical protein F56F10.2 hypothetical protein F56F10.2 hypothetical protein F5AC22E12. protein FZK11.4 [imported] iprotein FZK11.4 [imported] iprotein FZK11.4 [imported] iprotein fZK11.4 [imported] ippothetical protein GMSB [imported] ippothetical protein GMSB [imported] ippothetical protein F3DB.3 hypothetical protein F3DB.3 hypothetical protein T5C23.200 ippothetical prote
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receptor like protein - Arabidd
ES43 protein - barley
ES43 protein homolog F19H22.20C
ES43 protein homolog F19H22.20C
ES43 protein fimported] -
hypothetical protein YPL138C -
milo2 protein - fission yeast (s
probable phd finger transcripti
hypothetical protein F26H11.3a
hypothetical protein F26H11.3b
hypothetical protein F26H11.3b
ALR protein - human
ALR protein - human
hypothetical protein T32A16.30
probable molybopterin-guanine
probable transcription regulat
glucokinase regulator - African
hypothetical protein APE0614 -
hypothetical protein APE0614 -
hypothetical protein APE0614 -
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                                                           alignment_scores:
Quality:
                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
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seq_documentation_block:
    receptor like protein - Arabidopsis thaliana (fragment)
    N;Alternate names: protein AT4922140
    C;Species: Arabidopsis thaliana (mouse-ear cress)
    C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
    C;Accession: T49121
    R;Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemck submitted to the Protein Sequence Database, May 2000
    A;Reference number: Z25016
    A;Accession: T49121
    A;Status: preliminary
    A;Residues: 1-201 <BEV>
    A;Residues: 1-201 <BEV>
    A;Cross-references: EMBL:AL022140; GSPDB:GN00062; ATSP:AT4922140
    A;Experimental source: cultivar Columbia; BAC clone F1N20
    C:Genetics:
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pir2:T15670
pir2:S22412
pir2:S61299
A;Gene: ATSP:AT4g22140
A;Map position: 4
A;Note: intron position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor like protein (partial) [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (species: Arabidopsis thaliana (mouse-ear cress) (species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 (species) (spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-201 <S
A; Cross-references:
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US-09-684-016-48411 x C85253
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    Quality:
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          positions
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       not resolved
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Gaps: 0
Percent Identity: 91.304
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Ratio:

138.00 6.273 95.652

Percent Identity:

Length:

23 0 91.304

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A;Gene: ATSP:F19H22.200
A;Map position: 4
A;Introns: 25/1; 140/2; 163/2
                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-258 <BEV>
A; Cross-references: EMBL:AL035679; GSPDB:GN00062; ATSP:F19H22.200
A; Experimental source: cultivar Columbia; BAC clone F19H22
C; Genetics:
                                                                                                                                                                                                                                                                                          R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15184
A;Accession: T06070
A;Accession: T06070
                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ES43 protein homolog F19H22.200 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999
C;Accession: T06070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, February 1994
A; Reference number: S44281
A; Accession: S44281
A; Molecule type: mRNA
A; Residues: 1-227 <SPE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ES43 protein - barley
C; Species: Hordeum vulgare (barley)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C; Accession: $44281
R; Speulman, E; Salamini, F.
                                              alignment_scores:
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US-09-684-016-48411 x S44281
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US-09-684-016-48411 x T49121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 TyrCysLysCysGluMetProTyrAsnProAspAspLeuMetValGlnCy 131
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Ratio:
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                    position: 16L
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submitted to the EMBL Data Library, December 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome
A;Reference number: S69040
A;Accession: S69047
                                                                                                                                                                                                                                      C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
C;Accession: S69047
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Quality:
Ratio:
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seq_documentation_block:
ES43 like protein [imported] - Arabidopsis thaliana
C;Speciles: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: H85462
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, T)
Nature 402, 769-777, 1999
A; Gene: MIPS: YPL138c
                                           A;Cross-references: EMBL:U43703; NID:g1244769; PID:g1244777; GSPDB:GN00016; MIPS:YPL1
                                                                    A; Molecule type: DNA
A; Residues: 1-353 <HAL>
                                                                                                                                                                                                                    R; Hall, J.; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms,
                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                           seq_name: pir2:S69047
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A: Map position: 4
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                                                                                                                                                                                                                                                                                                                  hypothetical protein YPL138c - yeast (Saccharomyces cerevisiae)
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                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 78.261
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6
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                                                                                                                                                                       XVI left arm
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probable phd finger transcription regulator - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C;Accession: T41449
R;RRieger, M.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21994
A;Accession: T41449
A;Accession: T41449
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-424 RIE>
A;Cross-references: EMBL:AL031523; PIDN:CAA20664.1; GSPDB:GN00068; SPDB:SPCC594.05c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mlo2 protein - fission yeast (Schizosaccharomyces pombe)
(;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03.0pec.1999 #sequence_revision 03-Dec.1999 #text_change 03-Dec.1999
C;Accession: T40419
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D. submitted to the EMBL Data Library, October 1999
A;Reference number: Z21927
A;Accession: T40419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-684-016-48411 x T40419
                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                            seq_name: pir2:T41449
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A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL121863; PIDN:CAB58404.1; GSPDB:GN00067; SPDB:SPBC4.05
A;Experimental source: strain 972h-; cosmid c4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-329 < MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: pir2:T40419
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US-09-684-016-48411 x S69047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: S69047 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                           137 rMetPheGlnCysIleLeuCysGluAspTrp 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ArgPheCysIleCysAspThrValTyrAsnProGluThrGluGluGlyTh 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39
                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 AATGGCGCAATGCGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 CGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
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55.556
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4.156
69.565
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Gaps: 1
Percent Identity: 47.826
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1
44.444
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hypothetical protein F26H11.3c - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000 C;Accession: T21435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 2
A;Introns: 11/1; 42/3; 183/2; 243/2; 287/1
A;Introns: bromodomain homology
F;266-321/Domain: bromodomain homology <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, November 1996 A;Reference number: 219421 A;Accession: T21433
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
                                                                                                                                            seq_name: pir2:T21435
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A;Experimental source: clone F26H11
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A; Residues: 1-405 <WIL>
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                                                                                           seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-016-48411 x T21433
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                                                                                                                                                                                           188 sAspSerCysGlnGlyTrp
                                                                                                                                                                                                                                                                                    172 TyrCysValCysGlnLysProTyrAspAspThrLysPheTyrValGlyCy 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||:::|||||| ||||||| 133 uGlyCysAspGlyCysGluAspTrp 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 TyrCysIleCysGln......LysProAspAspGlySerTrpMetLe 133
                                                                                                                                                                                                                                       55 CGAGGGCTGCACTGACTGG 73
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                                                                                                                                                                                                                                                                                                                                5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
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4.429
60.870
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4.167
60.000
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Gaps:
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0
34.783
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A;Map position: 2
A;Introns: 116/1; 147/3; 288/2; 348/2; 392/1
C;Superfamily: bromodomain homology
F;371-426/Domain: bromodomain homology <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
hypothetical protein F78H11.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T21430
                                                                                                                                     alignment_block:
US-09-684-016-48411 x T21430
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A;Experimental source: clone F26H11
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A; Residues: 1-510 <WIL>
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A;Accession: T21430
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    Quality:
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A;Introns: 58/1; 89/3; 230/2; 290/2; 334/1
C;Superfamily: bromodomain homology
F;313-368/Domain: bromodomain homology <BRO>
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A;Experimental source: clone F26H11
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A;Accession: T21435
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                         Align seg 1/1
                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 sAspSerCysGlnGlyTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 TyrCysValCysGlnLysProTyrAspAspThrLysPheTyrValGlyCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 CGAGGGCTGCACTGACTGG 73
                         5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
TyrCysValCysGlnLysProTyrAspAspThrLysPheTyrValGlyCy 293
                                                                                                                                                                                                                              Quality:
Ratio:
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0
34.783
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0
34.783
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A; Map position: 12
C; Superfamily: human ALR protein
C; Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ALR protein - human
C;Species: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Accession: T03454
                                              alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated
A;Molecule type: mRNA
A;Residues: 1-5262 <PRA>
                                                                                                                                                                                                                                                                                                                                                                              R;Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Oncogene 15, 549-560, 1997
A;Title: Structure and expression pattern of human ALR, A;Reference number: Z14954; MUID:97388474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Map position: 12
C:Superfamily: human ALR protein
C:Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Ya Oncogene 15, 549-560, 1997
A;Title: Structure and expression pattern of human ALR, a novel gene with strong homo A;Reference number: Z14954; MUID:97388474
A;Accession: T03455
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US-09-684-016-48411 x T03455
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A;Molecule type: mRNA
A;Residues: 1-4957 <PRA>
                                                                                                                                                                                                                   A;Gene: ALR
                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AF010403; NID:g2358284; PIDN:AAC51734.1; PID:g2358285
                                                                                                                                                                                                                                                                                                                                                             A; Accession: T03454
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: ALR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T03455
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    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      946 sGluArgTrp 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 sAspSerCysGlnGlyTrp 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 CACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 TGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGAGGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                           a novel
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seq_documentation_block:
hypothetical protein T32A16.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dateis: Arabidopsis thaliana (mouse-ear cress)
C;Datei : I1-Jun-1999 #sequence_revision I1-Jun-1999 #text_change 22-Oct-1999
C;Accession: T08905
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16518
A;Accession: T08905
A;Molecule type: DNA
A;Residues: I-443 <-BEV >
A;Cross-references: EMBL:AL078468; GSPDB:GN00062; ATSP:T32A16.30
A;Experimental source: cultivar Columbia; BAC clone T32A16
C;Genetics:
A;Gene: ATSP:T32A16.30
A;Introns: 28/3; 81/3; 172/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-O
C:Accession: T25101
R:McMurray, A.
submitted to the EMBL Data Library, June 19
A:Reference number: Z19982
A:Recession: T25101
A:Status: preliminary; translated from GB/E
A:Molecule type: DNA
A:Residues: 1-416 <WILD
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hypothetical protein T22C1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 15-Oct-1999
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US-09-684-016-48411 x T25101
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Quality:
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US-09-684-016-48411 x T03454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 AATGGCGCAATGCGAGGGCTGCACTGACTGG 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uLeuLeuGlnCysGluIleCysGluAspTrp 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGAGGGCTG
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3.719
59.259
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Percent Identity: 37.037
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                                                                                                                                                                                                                                                                                             Mewes,
                                                                                                                                                                                                                                                                                           H.W.;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1588 <MUR>
A;Cross-references: EMBL:AL109739; NID:e1534774; PIDN:CAB52274.1; GSPDB:GN00066; SPDB;
A;Cxperimental source: strain 972h-; cosmid c343
                                                                                                                                                                                                          probable transcription regulator protein - fission C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 C;Accession: T38660
                                                                                                                    R;Murphy, L.; Harris, D.; Wood, V.; submitted to the EMBL Data Library, A;Reference number: Z21804
A;Accession: T38660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
A;Reference number: A81775; MUID:20222556
A;Accession: B81911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: B81911
R;Parkhill, J.; Achtman, M.; James, Holroyd, S.; Jagels, K.; Leather, Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable molybdopterin-guanine dinucleotide biosynthesis protein A NMA1417 [imported]
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84657.1; PID:g738
A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-192 < PAR>
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US-09-684-016-48411 x T08905
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                                                                                                                                                                                                                                                                                                                                                 seq_name: pir2:T38660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: pir2:B81911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 TyrCysThrCysAspArgProTyr...ProAspProAsnValGluGluGl 143
                                                                                                                                                                                                                                                                                                                                                                                                                                              14 TGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 ....CTAATGGCGCAATGCGAGGGCTGCACTGACTGG
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4.250
48.276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K.D.; Bentley, S.D.; Churcher, C.; Klee,
S.; Moule, S.; Mungall, K.; Quail, M.A.;
                                                                                                                                                                 August
                                                                                                                                                                    Rajandream,
August 1997
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66.667
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2
44.828
                                                                                                                                                                                                                                                                                 yeast (Schizosaccharomyces
                                                                                                                                                                                                                                    #text_change 03-Dec-1999
                                                                                                                                                                                         Barrell,
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                                                                                                                                                                                                                                                                                                                                                                                                      114
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Rajandre
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SPDB:SPAC343.11c

pombe)

A; Map position:

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hypothetical protein APE0614 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H72647
R;Kawarabayasi, Y; Hino, Y; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status, r-v--.
A;Nolecule type: mRNA
A;Residues: 1-619 <VEI>
A;Cross-references: EMBL:X80901; NID:g556677; PIDN:CAA56863.1; PID:g556678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A72450; A; Accession: H72647
                                                           A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy. A; Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-684-016-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Cloning and expression of a Xenopus liver cDNA encoding a A; Reference number: S48729; MUID:95010134
A; Accession: S48729
A; Molecule type:
                       A;Status:
                                                                                                                                                                                                                                                  seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-684-016-48411 x T38660
                                                                                                                                                                                                                                                                                      seq_name: pir2:H72647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1473 sAsnCysLeuGluTrp 1478
                                                                                                                                                                                                                                                                                                                                                                                                                 341
                                                                                                                                                                                                                                                                                                                                                                         50
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                                                                                                                                                                                                                                                                                                                                                                       CAATGCGAGGGCTGCACTGACTGGTAAGTTTCAC 83
                                                                                                                                                                                                                                                                                                                                                                                                             GlyIleMetAspAlaValGluCysValProThrTyrGlnAlaAspTrpAr 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTATTGTAAAT...GTGAGATGCCTTACAACCCTGATGACCTAATGGCG
                                                                                                                                                                                                                                                                                                                                gAspValArgGlyPheIleThrGlyGlyTyrHis 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
                       preliminary
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Ratio:
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Ratio:
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2.568
78.571
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3.562
72.727
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6
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36.364
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1
39.286
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                                                                                                                                              Takal
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seq_documentation_block:
hypothetical protein YH9C.2 - Caenorhabditis elegans
c;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-1288 <test>
A;Residues: 1-1288 <test>
A;Cross-references: EMBL:U70825; NID:g1732064; PID:g1732065; PIDN:AAC52955.1
A;Experimental source: strain Sprague-Dawley; kidney
C;Superfamily: hypothetical protein YKL215c
C;Keywords: homodimer; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5-oxoprolinase (ATP-hydrolyzing) (EC 3.5.2.9) - rat
N;Alternate names: pyroglutamase (ATP-hydrolyzing)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000
C;Accession: T42756
R;Ye, G.J.; Breslow, E.; Meister, A.
J. Biol. Chem. 271, 32293-32300, 1996
A;Title: The amino acid sequence of rat kidney 5-oxo-L-prolinase determined by cDNA c
A;Reference number: Z22263; MUID:97113037
A;Accession: T42756
C;Accession: T26971
R;Harris, B.
                                                                                                                                                                                  seq_name: pir2:T26971
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A;Cross references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79584.1; PID:d1043370; PID:g
A;Experimental source: strain K1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: T42756 from: 1 to: 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                         215 HisValSerLeuSerSerGluValMetProMetValArgIleValProAr 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 TGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTACCAGTCA
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                                                                                                                                                                                                                                                                                      42 AGGTCATCAGGGTTGTAAGGCATCTCACATTTACAATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 GTGCAGCCCTCGCATTGCGCCATTAGGT 39
                                                                                                                                                                                                                                                                                                                                                                                          CATGTGAAACTTACCAGTCAGTGCAGCCCT.....CGCATTGCGCCATT 43
                                                                                                                                                                                                                                     gGlyHisThrAlaCysAlaAspAlaTyrLeuThrProThr 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
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2.800
66.667
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3.111
69.231
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Gaps:
Percent Identity:
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38.462
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alignment_block:
US-09-684-016-48411 x T32633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F15E6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32633
R;Miller, N.; Stellyes, L.; Bradshaw, H.; Keppler, D.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F15E6.
A;Reference number: Z21202
A;Accession: T32633
                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 4
A; Introns: 16/1; 68/1; 190/3; 301/2; 602/3; 1203/3; 1295/1; 1554/3; 1642/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1655 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: CESP:Y47H9C.2
A;Map position: 1
A;Introns: 83/2; 142/1; 194/1; 234/1; 262/2; 284/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-368 <WIL>
A;Cross-references: EMBL;AL032657; PIDN:CAA21738.1; GSPDB:GN00019; CESP:Y47H9C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP:F15E6.1
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A;Reference number: 20293
A;Accession: 72697
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                   Align seg 1/1 to: T32633 from: 1
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836 uGlyCysLysThrTrp 841
                                                                                                    821 CysHisCysGlyMetAspHisGlyAspGlyAspThrIle...GluCysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 GluHisValLysMetLysTyrCysThrThrCysArgLeuTyrArgProPr 175
                                                  58 GGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 GCAGCCCTCGCATTGCGCCATT 43
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                                                                                                                                                 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oArgCysSerHisCysAlaIle 182
                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
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3.438
66.667
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4.192
59.091
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Gaps: 0
Percent Identity: 45.833
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                                                                                                    . 836
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A;Molecule type: DNA
A;Residues: 1-46;47-64;65-101;102-118;119-132;133-147;148-161;162-173;174-185;186-19
A;Cross-references: GB:M89923
C;Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: An analysis of the complete sequence of a sugarcane bacilliform virus genome A;Reference number: PQ0542; MUID:93139779
A;Accession: PQ0542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyprotein - sugarcane bacilliform virus (fragments)
C;Species: sugarcane bacilliform virus
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
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A;Residues: 1-180 <SHE>
C;Keywords: glycoprotein; hydrolase; transmembrane protein
C;Keywords site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Shelness, G.S.; Kanwar, Y.S.; Blobel, G.
J. Biol. Chem. 263, 17063-17070, 1988
A;Title: cDNA-derived primary structure of the glycoprotein component of canine A;Reference number: A31788; MUID:89034208
A;Accession: A31788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
seq_documentation_block:
signal peptidase (EC 3.4.99.-) (SPC 22/23) - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 21-May_1990 #sequence_revision 21-May-1990 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                      alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Bouhida, M.; Lockhart, B.E.L.; Olszewski, N.E.
J. Gen. Virol. 74, 15–22, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: pir2:A31788
                                                                                                                                                                                             Align seg 1/1 to: PQ0542 from: 1 to: 199
                                                                                                                                                                                                                                             US-09-684-016-48411 x PQ0542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 sSerCys 65
                                               58 GGGCTGC 64
                                                                                               47 CysArgCysTyrValCysGlySerProAspHisLeuMetLysAspCysLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 AspIleThrAlaAspLeuGluAsnIlePheAspTrpAsnValLysGlnLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGT
                                                                                                                         8 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uPheLeuTyrLeuSerAlaGluTyrSerThrLys 96
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Ratio:
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3.786
73.684
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2.650
71.429
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Gaps: 0
Percent Identity: 42.857
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Percent Identity:
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42.105
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seq\_name: pir2:B86073

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seq_documentation_block:
hypothetical protein mobA [imported] - Escherichia coli (strain 0157:H7)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: B86073
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                     A:Cross-references: EMBL:L19201; NID:g304961; PIDN:AAB02992.1; PID:g304963
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A: Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: E65190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G;Date: 06-Oct-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999 C;Accession: S40803; E65190 Burland, V.; Daniels, D.L.; Blattner, F.R. Nucleic Acids Res. 21, 3391-3398, 1993 A;Reference number: S40802; MUID:93347969 A;Accession: S40803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    molybdopterin-guanine dinucleotide biosynthesis protein A - Escherichia coli N;Alternate names: mob protein C;Species: Escherichia coli
                                                                                alignment_scores:
                                                                                                                                                                   A;Gene: mobA
A;Start codon: GTG
                                                                                                                                                                                                                                                 A;Cross-references: GB:AE000461; GB:U00096; NID:g2367318; PIDN:AAC76855.1; PID:g1790288
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-194 <BLAT>
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US-09-684-016-48411 x B86073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: B86073
                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-194 <PLU>
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A; Residues: 1-194 <STO>
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  Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheCysProCysAspThrProTyrIleProHisAspLeuAlaAlaArg 112
                                                      Quality:
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4.727
68.750
52.00
4.727
68.750
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  Gaps:
Percent Identity:
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Percent Identity:
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6
                                                      Length:
16
0
50.000
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  A;Cross-references:
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seq_documentation_block:
ABC transporter, ATP-binding protein homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 02-Feb-2001
C;Accession: H70109
                                                                                                                                                      C;Accession: T41530
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, submitted to the EMBL Data Library, March 1999
                                                                                                                                                                                                                                                     C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: ATP; nucleotide binding; P-loop
F;38-235/Domain: ATP-binding cassette homology <ABC>
F;55-62/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943
A;Accession: H70109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
A; Molecule type: DNA
A; Residues: 1-721 < WOO>
                                                                                              A; Reference number: A; Accession: T41530
                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
hypothetical protein SPCC645.13 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain B31 C; Superfamily: unassigned ATP-binding cassette proteins;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-240 <KLE>
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US-09-684-016-48411 x S40803
                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: pir2:T41530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 sGlyGluPheIleSerIleGlnGlyLysSerGlyCysGlyLysSerThrL 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 AsnLysThrLysIleGlnValIleGluAsnLeuAsnLeuThrValGluLy 47
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PID:9268

EMBL: AL049498; PIDN: CAB39909.1; GSPDB: GN00068;

SPDB: SPCC645.13

972h-; cosmid c645

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C;Superfamily: sucrose synthase; 'sucrose/sucrose-phosphate synthase homology C;Keywords: glycosyltransferase; hexosyltransferase F;282-757/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Buchner, P. submitted to the EMBL Data Library, October 1997 A; Reference number: Z15720 A; Accession: T06497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable sucrose synthase (EC 2.4.1.13) 2 - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Accession: T06497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain C; Genetics:
seq_name: pir2:T16487
                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-684-016-48411/rev x T06497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
    Quality:
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A; Residues: 1-809 <BUC>
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US-09-684-016-48411 x T41530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: SPDB: SPCC645.13
                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: T06497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: T41530 from: 1
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                                                                                                                                                                                                                                                                                            457
                                        507 GlyLeuTyrArgValValHis 513
                                                                                                                          490
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tAsnAsnAlaAspPheIleIleThrSerThrTyrGlnGluIleAlaGlyT 490
                                                                                                                                                                                                                                                                                   GluAspLysTyrHisPheSerCysGlnPheThrAlaAspLeuIleAlaMe 473
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                                                                                                                          hrLysAsnThrIleGlyGlnTyrGluSerHisThrAlaPheThrLeuPro 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCTGCACTGACTGG 73
                                                                                 GGGTTGTAAGGCATCTCACAT 13
                                                                                                                                                               .....ACTTACCAGTCAGTG.....
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2.364
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Gaps: 2
Percent Identity: 26.316
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36.364
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A;Cross-references: GB:M29004; NID:g161463; PID:g161464
A;Note: the publication does not report the complete sequence
C;Superfamily: unassigned EGF-related proteins; EGF homology
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-325/Product: exogastrula-inducing protein #status predicted <EGIP>
F;47-104/Product: EGIP petide C #status predicted <EGIC>
F;52-90/Domain: EGF homology <EG1>
F;106-156/Product: EGIP petide D #status predicted <EGID>
F;111-151/Domain: EGF homology <EG2>
F;117-228/Product: EGIP petide A #status predicted <EGIA>
F;182-223/Domain: EGF homology <EG3>
F;250-309/Product: EGIP petide B #status predicted <EGIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Yang, Q.; Angerer, L.M.; Angerer, R.C. Science 246, 806-808, 1989
A; Title: Unusual pattern of accumulation of mRNA encoding A; Reference number: A40084; MUID:90049203
A; Accession: A40084
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exogastrula-inducing protein (EGIP) precursor - sea urchin (Strongylocentrotus purpun N;Alternate names; epidermal growth factor-related protein N;Contains: EGIP peptide A; EGIP peptide B; EGIP peptide C; EGIP peptide D C;Species: Strongylocentrotus purpuratus (purple urchin) C;Species: 20-Mar-1992 *sequence_revision 15-Aug-1997 *text_change 11-Jan-2000
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A;Introns: 21/3; 45/2; 100/3; 147/3; 177/3; 232/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F56F10.2
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 04-Mar-2000
C;Accession: T16487
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A; Residues: 1-325 <YAN>
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US-09-684-016-48411/rev x T16487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: A40084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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cosmid F56F10
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32.432
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C; Accession: D9660
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, C.A.; Li, Y.; Liu, X.; Liu, X.X.; Liu, Z.A.; Luros, J. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
                                                                                                                                                                                                                seq_documentation_block:
protein F2K11.14 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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submitted to the EMBL Data Lib
A;Reference number: Z21775
A;Accession: T38168
                                                                                                                                                                                                                                                                                                                                  seq_name: pir2:D96660
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US-09-684-016-48411 x T38168
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R; Devlin, K.; Church
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seq_documentation_block:
hypothetical protein SPAC22E12.11c - fission yeast (Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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US-09-684-016-48411 x A40084
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    Quality:
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A; Residues: 1-859 <DEV>
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Percent Similarity:
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Percent Similarity:
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Library, March 1996
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Gaps:
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: 64.286
                                                                                                                                               iel, N.A.; Kaul,
Conway, A.R.; C
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                      Southwick,
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                                                                                                                                                 l, S.; White, O.;
Creasy, T.H.; Dev
                        A.M.; Sun, H.; Tallon,
                                                               Khaykin, E.; Kim, C
Maiti, R.; Marziali
                                                                                                                                                     Dewar,
                                                                                                                                                     Alonso,
    71
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F;256-292/Domain: EGF homology <EG4>F;52-65,59-75,77-90,111-124,118-137,139-151,182-195,189-209,211-223,256-269,263-278,280
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A;Accession: D96660
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1518 <STO>
A;Cross-references: GB:AE005173; NID:g6633837; PIDN:AAF19696.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, A; Reference number: Z20245 A; Accession: T26611
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R; McMurray, A.
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A; Residues: 1-95 <WIL>
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US-09-684-016-48411 x D96660
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A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL023835; PIDN:CAA19489.1; GSPDB:GN00022; CESP:Y37A1B.4
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                                                                                                                                                                               122 GTTGTGTGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTAC
22 CATCTCAC 15
                                                                                     72 CAGTCAGTGCAGCCCTCGCATTGCGCCATTAGGTCATCAGGGTTGTAAGG
                                                                                                                                  46 IleLeuTrpAsnAsnIleLeuValMetIle.....
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                                        ....GlnCysAspGlyAsnIleLeuProGlnLysHisGlnGlyPheTyrA 71
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46/2; 84/3
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65.217
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39.130
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rgPheHis

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C;Species: Escherichia coli (;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C;Accession: B85615 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, 11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: terminal reductase during anaerobic growth on various sulfoxide are A; Note: chain A binds molybdopterin, chain B is an eletronen transfer protein, are C; Superfamily: nrfC protein; ferredoxin 2 (4Fe-45) homology C; Keywords: 4Fe-4S; heterotrimer; iron-sulfur protein; metalloprotein; oxidoreduce; 2-205/Product: dimethylsulfoxide reductase chain B #status experimental <MAT>F; 7-87/Domain: ferredoxin 2 (4Fe-4S) homology <FERI>F; 92-153/Domain: ferredoxin 2 (4Fe-4S] homology <FERI>F; 92-153/Domain: ferredoxin 2 (4Fe-4S] homology <FERI>F; 14, 17, 20, 79/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted F; 24, 67, 70, 75/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted F; 99, 102, 105, 145/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted F; 109, 126, 129, 141/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 20 min C;Complex: heterotrimer; chains A, B, and C;Function:
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A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: F64828
                                                                                                                                                                                                                                                                              seq_name: pir2:B85615
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A;Residues: 1-170, 'RA',171-205 <BIL>
A;Cross-references: GB:J03412; NID:gl
A;Note: part of this sequence, included
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                                                                                                                                                                        hypothetical protein dmsB [imported] -
                                                                                                                                                                                                               seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                             rLysGlyHisMetThrLysCysAspGlyCysTyrAsp
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                                                                                                                                                                           Escherichia coli (strain 0157:H7)
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   J.D.; Rose, Potamousis,
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       D.J.;
K.; A
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   Apodaca,
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   seq_name: pir2:T04224
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A;Map position: 5
A;Introns: 61/1; 83/3
C;Superfamily: Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F32D8.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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US-09-684-016-48411 x B85615
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A; Residues: 1-245 <WIL>
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A; Accession: T21654
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A; Residues: 1-205 <STO>
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                                                                                                                                                                       Align seg 1/1
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                                          52 ATGCGAG...GGCTGCACT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 .....ATGGCGCAATGCGAGGGCTGCACTGAC 70
                                                                                       71 HisCysAlaCysGluSerThrCysAsnAsnProAspProTyrCysSerLy
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                                                                                                                               5 TATTGTAAATGTGAGATGCCT...TACAACCCTGATGACCTAATGGCGCA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CESP: F32D8.3
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sCysGluProGlyCysThr 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgTyrCysHisMetAlaCysProTyrGlyAlaProGlnTyrAsnGluTh
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Ratio:
                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                           to: T21654 from:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                             51.00
3.643
60.870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.00
3.400
51.724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterohemorrhagic Escherichia coli 0157:H7 MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                             elegans
                                                                                                                                                                                                                                                                                  Percent Identity:
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                                                                                                                                                                                                                                                                                                  Gaps:
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1
34.483
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seq_name: pir2:F71844
                                                                                                                                                                                                                                                             alignment_block:
US-09-684-016-48411/rev x A35291
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M37901; NID:g211094; PIDN:AAA48574.1; PID:g211095 C;Superfamily: fumarate hydratase C;Keywords: amidine-lyase; carbon-nitrogen lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Aimi, J.; Badylak, J.; Williams, J.; Chen, Z.; Zalkin, H.; Dixon, J.E.
J. Biol. Chem. 265, 9011-9014, 1990
A;Title: Cloning of a cDNA encoding adenylosuccinate lyase by functional complementation A;Reference number: A35291; MUID:90264380
A;Accession: A35291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-684-016-48411 x T04224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: T5C23.200
C; Superfamily: caffeoyl-CoA 3-O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: Z15261
A;Accession: T04224
A;Molecule type: DNA
A;Residues: 1-396 <BEV>
A;Cross-references: EMBL:AL049500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; submitted to the Protein Sequence Database, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-459 < AIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir2:A35291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: cultivar Columbia; BAC clone T5C23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T5C23.200 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T04224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: T04224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                            58
                                             74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 TGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGAGGGC
                                             sProLysAlaAlaIleIleHisLeuGlyAlaThrSerCysTyrVal
                                                                                   CCCTCGCATTGCGCCATTAGGTCATCAGGGTTGTAAGGCATCTCACATT 12
                                                                                                                              LysLeuArgHisAspValMetAlaHisValHisThrPheAlaHisCysCy 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CysAsnMetProTyrLeuProAspAspLeuLeuAsnIleLeuGly 25
                                                                                                                                                                                                                                                                                                                                                                            Quality:
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                                                                                                                                                                                                                       to: A35291 from: 1
                                                                                                                                                                                                                                                                                                                               51.00
2.550
60.606
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4.250
75.000
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Gaps: 0
Percent Identity: 56.250
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                                                                                                                                                                                                                       to: 459
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6
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0
27.273
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                                                               alignment_scores:
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein AAG21600.1 [imported] - Arabidopsis thaliana
(;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H86457
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Creasy, T.H.; Dewar, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
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A; Molecule type: DNA
A; Residues: 1-578 <ARN>
A; Cross-references: GB:AE001541; GB:AE001439; NID:g4155724; PIDN:AAD06712.1;
A; Cross-references: Strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: F71844
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric p A;Reference number: A71800; MUID:99120557
A;Accession: F71844
A;Map
                                                                                                      A; Molecule type: DNA
A; Residues: 1-697 <STO>
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US-09-684-016-48411/rev x F71844
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Quality:
Ratio:
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                                                                     A;Cross-references: GB:AE005172; NID:g10645488; PIDN:AAG21600.1; GSPDB:GN00141
                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: pir2:H86457
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C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 17-Mar-2000
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C;Species: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
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ABC transporter, ATP-bin
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                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 yGlnLysIleAlaLeuIleGlyHisSerGlyCysGlyLysSer 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 LysSerLysHisProValLeuLysAsnPheAsnLeuThrIleGlnLysGl 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  jhp1129
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2.684
61.290
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0
38.710
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Ratio: Percent Similarity:

Quality:

51.00 3.643 50.000

Length: 28
Gaps: 1
Percent Identity: 35.714

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R:Pauley, A.
submitted to the EMBL Data Library, July 1995
A:Description: The sequence of C. elegans cost
A:Reference number: Z18386
A:Accession: T15670
Biochem. J. 282, 447-452, 1992

A; Title: Molecular cloning of a cDNA encoding the glycoprotein of hen ovi A; Reference number: S22412; MUID:92189580

A; Accession: S22412

A; Molecular type: mRNA
A; Residues: 1-180 <NEW1>
A; Cross-references: EMBL:X60795; NID:g63421; PIDN:CAA43208.1; PID:g63422
                                                                                                                                                                                                                                        C;Species: Gallus gallus (chicken)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jul-2000
C;Accession: S22412; S40018; S15551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: CESP:C27H5.5
A;Introns: 27/2; 93/3; 203/1; 336/1; 358/2; 394/3; 473/2; 489/3; 531/3; 574/2; 636/3; 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-1332 <PAU> A;Cross-references: EMBL:U14635; NID:g540265; PID:gA;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C27H5.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15670
                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
signal peptidase (EC 3.4.99.-), microsomal - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-684-016-48411/rev x T15670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                               R; Newsome, A.L.; McLean, J.W.; Lively, M.O. Biochem. J. 282, 447-452, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: pir2:S22412
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US-09-684-016-48411 x H86457
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              622 pGlyCysGlyValTrp.....HisHisThrArg 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAATACC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gTyrProMetAspHisGlnAsnCysGluIleAlaPheAlaSerTyrAlaT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCACCTTACATGTGAAACTTACCAGTCAGTGCAGCCCTCGCATTGCG..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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2.196
63.889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 36
Gaps: 3
Percent Identity: 36.111
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                                                                                                                                                    the glycoprotein of hen oviduct microsomal
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seq_documentation_block:
lipopolysaccharide heptosyltransferase (EC 2.4.99.-) II rfaF [similarity] - |
C;Species: Neisseria gonorrhoeae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C;Accession: S61299
R;Schwan, E.T.; Robertson, B.D.; Brade, H.; van Putten, J.P.M.
Mol. Microbiol. 15, 267-275, 1995
Mol. Microbiol. 17aF mutants express Rd(2) chemotype LPS and do not enter
A;Pitle: Gonococcal rfaF mutants express Rd(2) chemotype LPS and do not enter
A;Accession: S61299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:237141; NID:g599919; PIDN:CAA85504.1; PID:g599920 A;Note: the sequence of residues 1-2 are not shown in this paper C;Superfamily: ADP-heptose--LPS heptosyltransferase II C;Keywords: glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S40018
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-15;36-45;50-58;76-83;97-118;141-160 <NEW2>
A;Residues: 1-19;36-45;50-58;76-83;97-118;141-160 <NEW2>
C;Keywords: glycoprotein; hydrolase; transmembrane protein
F;1-180/Product: signal peptidase #status experimental <MAT>
F;141/Binding site: carbohydrate (Asn) (covalent) #status experimental
seq_documentation_block:
lipopolysaccharide heptosyltransferase (EC
C;Species: Neisseria meningitidis
                                                                                                             seq_name: pir2:B81869
                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-684-016-48411/rev x S61299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-336 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: S61299 from: 1 to: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-684-016-48411 x S22412
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                                                                                                                                                                         307
                                                                                                                                                                                                                                                                                                           293 AspArgAlaLysIle...ValSerLeuHisLeuGlu...CysSerProCy
                                                                                                                                                                                                   63 CAGCCCTCGCATTGCGCCATTAGGTCATCAGGGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : ||||||||||::: |||||||||||::: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 AAGGTGATACTTATCTTCAATTTATTCCACACAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 AspIleThrAlaAspLeuGlnSerIlePheAspTrpAsnValLysGlnLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGT
                                                                                                                                                                   sPheLysArgGluCysProLeuGlyHisThrAspCys 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pir2:S61299
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Gaps: 0
Percent Identity: 39.286
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C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001 C;Accession: B81869

2.4.99.-) II NMA1727 [similarity] -

Neissa

J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee,

S.R.;

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34

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Swissprot_39:OPLA_RAT - Swissprot_39:IFIP_IUMAN - Swissprot_39:IFIP_IUMAN - Swissprot_39:MOBA_ECO57 + Swissprot_39:MOBA_ECO57 + Swissprot_39:MOBA_ECO57 + Swissprot_39:MOBA_ECO57 + Swissprot_39:MOBA_ECOLI + Swissprot_39:MOFA_HUMAN + Swissprot_39:MOFA_HUMAN + Swissprot_39:MOFA_HUMAN - Swissprot_39:MOFA_HUMAN - Swissprot_39:MOFA_HUMAN + Swissprot_39:MOFA_HUMAN + Swissprot_39:MOFA_HUMAN + Swissprot_39:MOFA_HUMAN - Swissprot_39:MOFA_HUMAN - Swissprot_39:MOFA_HUMAN - Swissprot_39:MOFA_MOUSE + Swissprot_39:MOFA_MOUSE + Swissprot_39:MOFA_MOUSE + Swissprot_39:MOFA_MOUSE - Swissprot_39:MOFA_CHICK + Swissprot_39:MOFA_CH
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SwissProt_39:GCKR_XENLA +
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SwissProt_39:MLO2_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database: SwissProt_39:*
Database sequences: 100059
Database length: 36664827
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Database: Swi
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Query: US-09-684-016-48411
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-Q-/c9n2_1/USPTC_spool/US99684016/runat_19032002_084440_20960/app_query.fasta_1.182
-Q-/c9n2_1/USPTC_spool/US99684016/runat_19032002_084440_20960/app_query.fasta_1.182
-DB=Swissprot_39 -QFMT=fastan -SUFFIX=std.rsp -GAPOP-12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPEXT=4.000 -GAPEXT=0.000 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALICN=200 -THR_SCORE-PCt
-THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE-LOCAL -OUTFHT-Pfs
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USEP=US09684016_@CGA1_1_28 -NOPU=6 -ICPU=3 -LONGLOG
-DEV -THROUTH-170 - ALIGN=45 -NOPU=6 -ICPU=3 -LONGLOG
-DEV -THROUTH-170 - ALIGN=45 -NOPU=6 -ICPU=3 -LONGLOG
-DEV -THROUTH-170 -NAXLEN-200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
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                                    ZSCORE ESCORE Len
50 161.74 0.0747
50 161.74 0.0747
1.80 0.7099
55 132.34 1.80
1.50 131.97 1.81
0 124.61 2.23
1.00 129.17 8.26
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2.00 124.32 11.36
251.00 131.62 11.36
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251.00 131.62 11.36
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250.00 114.36 17.53
250.00 112.47 17.87
250.00 122.38 29.
48.50 105.95 18.57
29.48 29.00 112.30 24.4
48.50 109.02 25.
48.50 108.96 30.0
48.50 109.02 25.
48.50 109.03 32
3.4 48.00 112.88 3
3.6 48.00 113.46 3
3.7 48.00 113.46 3
3.8 48.00 113.57
252 48.00 112.57
252 48.00 112.57
SwissProt_39:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                        137 rMetPheGlnCysIleLeuCysGluAspTrp 147
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SwissProt_39:NGER_RAT +
SwissProt_39:AC3_HUMAN -
SwissProt_39:MM17_HUMAN -
SwissProt_39:APC2_CAVPO +
SwissProt_39:EGIP_ANTCR +
                                                                                                                                                                                                                                                                                      alignment_scores:
Quality:
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                                                                                                                               Align seg 1/1
                                                                                                                                                                           US-09-684-016-48411 x MLO2_SCHPO
                                                                                                                                                                                                                                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00628; PHD; 1.
Pfam; PF02207; zf-UBRI; 1.
SMART; SM002249; PHD; 1.
SMART; SM00396; ZnF_UBRI; 1
SEQUENCE 329 AA; 38078 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McDougall R.C., Rajandream M.A., Barrell B.G., Brown S., Harris D.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: NOT KNOWN, INTERFERE WITH MITOTIC CHROMOSOME SEGREGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97128260; PubMed-8972853;
Javerzat J.-P., Cranston G., Allshire R.A.;
"Fission yeast genes which disrupt mitotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seg
20-AUG-2001 (Rel. 40, Last ann
                                           121 ArgPheCysIleCysAspThrValTyrAsnProGluThrGluGluGlyTh 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001965; PHD.
InterPro; IPR003126; ZnF_UBR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L42550; AAB41271.1; -. EMBL; AL121863; CAB58404.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4896;
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MLO2 OR SPBC4.05
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43 AATGGCGCAATGCGAGGGCTGCACTGACTGG 73
                                                                               2 AGGTATTGTAAATGTGAGATGCCTTACAACCCT.....GATGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WHEN OVEREXPRESSED.
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                                                                                                                               to: MLO2_SCHPO from: 1
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                                                                                                                                                                                                                                           65.50
4.367
55:556
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Q99928 homo sapiens (hum
Q99129 homo sapiens (hum
Q90129 homo sapiens (hum
P27916 cavia porcellus (
P15217 anthocidaris cras
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seq\_name:

SwissProt\_39:MOBA\_NEIMA

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Seq_documentation_block:

ID MOBA_NEIMA STANDA
AC Q9JUA5;
DT 20-AUG-2001 (Rel. 40,
DT 20-AUG-200
alignment_block:
US-09-684-016-48411 x MOBA_NEIMA
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RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;

ROmplete DNA sequence of a serogroup A strain of Neisseria

meningitidis 22491.";

RE MATURE 404:502-506(2000).

C. FUNCTION: LINKS A GUANOSINE 5'-PHOSPHATE TO MOLYDOPTERIN (MPT)

C. FUNCTION: LINKS A GUANOSINE 5'-PHOSPHATE TO MOLYDOPTERIN (MPT)

C. I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

C. I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                O31314;
15-JUL-1998 (Rel. 36, Created)
15-DEC-1998 (Rel. 37, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
CELL DIVISION PROTEIN FTSZ (75 KDA ANT
                                                                                                                                                                                                                                                                                                      documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Bartonellaceae;
                                Bacteria;
                                                   Bartonella bacilliformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL162755; CAB84657.1; -. Molybdenum cofactor biosynthes
                                                                                                                                                                                                                                                                         FTSZ_BARBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-22491 / SEROGROUP A / SEROTYPE MEDLINE-20222556; Pubmed-10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                CysAspMetProTyrLeuProAspAspLeuValAlaArgPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE MOBA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                   SwissProt_39:FTSZ_BARBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                         Proteobacteria;
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                                                                                                                                                                                                                                                                            STANDARD;
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Bartonella
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4.538
86.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biosynthesis; GTP-binding; Complete proteome. 21803 MW; 005C495C6C64D290 CRC64;
                      alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent
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                         subdivision;
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Gaps:
Identity:
                                                                                                                ce update)
tion update)
A ANTIGEN).
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: 0
: 66.667
                         Rhizobiaceae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN A.
                      group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
GCKR_XENLA STAN
Q91754;
Q17-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
30-MAY-2000 (Rel. 3
                                                                                                                       .documentation_block:
    GCKR_XENLA STANDARD;
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NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            521 oGluAlaArgLeuGluProAlaValLysProLeuGlnAsnGlu.....
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PROSITE; PS01134; FTSZ_1; 1.
PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000158; FtsZ.
InterPro; IPR003008; Tubul
Pfam; PF00091; tubulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.
-!- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).
-!- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 GTGTGGAATAAATTGAAGATAAGTATCACCTTA.....CATGTGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF007266; AAC
HSSP; Q57816; 1FSZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restricted the succession of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Padmalayam I., Anderson B., Kron M., Kelly T., Baumstar "The 75-kilodalton antigen of Bartonella bacilliformis structural homolog of the cell division protein ftsz."; J. Bacteriol. 179:4545-4552(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97369823; PubMed=9226264; Padmalayam I., Anderson B., Kron M.,
                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                         75
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACCAGTCAGTGCAGCCCTCGCATTGCGCCCATTAGGTCATCAGGGTTGTA 26
                                                                                                                                                                                                                                                                                                                                     AGGCATCTCACATTTACAAT
                                                                                                                                                                                                          SwissProt_39:GCKR_XENLA
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                                                                                                                                                                                                                                                                           .GluSerHisIleTyrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
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107 115 GTP (POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTSZ_BARBA
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2.173
65.000
   . 35, Created)
. 35, Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63503 MW;
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                                                                                                                             PRT;
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C32007DADCD2D75B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                             619
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                                                                                                                                                                                                                                                                                                                                                                                               535
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its

Last sequence up

update)

update)

GLUCOKINASE REGULATORY PROTEIN

(GLUCOKINASE REGULATOR).

frog).

Xenopus laevis (African clawed

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seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
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                                                                                                                                                                                P97608;
15-DEC-1998
15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                            documentation_block:
                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                            SEQUENCE FROM N.A., AND PARTIAL SEQUE STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                            357
                                                                                                                                                                                                                                                                                                                                                                                   OPLAH.
                                                                                                                                                                   5-OXOPROLINASE
                                                                                                                                                                                                                                             OPLA_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD025295; GCKR; 1.
PROSITE; PS01272; GCKR; 1.
SEQUENCE 619 AA; 68738 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):
                 MEDLINE-97113037;
                                                                           NCBI_TaxID=10116;
                                                                                                                                                   (5-OPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001741; GCKR. InterPro; IPR001347; SIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X80901; CAA56863.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphate-insensitive regulatory protein of glucokinase.";
Eur. J. Biochem. 225:43-51(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Veiga-Da-Cunha M., Detheux M., Watelet N., van Schaftingen ^nCloning and expression of a Xenopus liver cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95010134; PubMed=7925465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01380; SIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                         50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE SIS FAMILY. GCKR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: INHIBITS GLUCOKINASE BY FORMING AN INACTIVE
 <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                        CAATGCGAGGGCTGCACTGACTGGTAAGTTTCAC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity:
                                                                                                                                                                                                                                                                                                                           gAspValArgGlyPheIleThrGlyGlyTyrHis 368
                                                                                                                                                                                                                                                                                                                                                                                                                 GGTATTGTAAAT...
                                                                                                                                                                                                                                                                                         SwissProt_39:OPLA_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
 Breslow
                                                                                                                                                           (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
(Rel. 37, Last annotation update)
(ASE (EC 3.5.2.9) (5-0XO-L-PROLINASE) (PYROGLUTAMASE)
                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.50
2.568
78.571
PubMed=8943290;
E., Meister A.;
                                                                                                                                                                                                                                                                                                                                                                                                                   . GTGAGATGCCTTACAACCCTGATGACCTAATGGCG
                                                                                          Rodentia;
                                                                                                        Chordata;
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                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41B72C1981D1BA52 CRC64;
                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 28
Gaps: 1
Identity: 39.286
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                                                                                          Rattus
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alignment_block: US-09-684-016-48411/rev \times OPLA_RAT
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                                                                                                                                                                                                                                                           HIP1_HUMAN
000291; 000
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SEQUENCE
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           candidate gene in a CAG expansion.";
                                                        SEQUENCE FROM N.A.
Huq A.H.M.M., Nichol
Hayden M.R.;
                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
                                                                                                                                             Homo sapiens (Human).

Homo sapiens (Human).

Metazoa; Chordata;
                                                                                                                                                                                HIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U70825; AAC52955.1; InterPro; IPR002821; Hydantoinase_A. InterPro; IPR003692; Hydantoinase_B. Pfam; PF01968; Hydantoinase_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ye G.-J., Breslow E., Meister A.;
J. Biol. Chem. 272:4646-4646(1997).
-i- FUNCTION: CATALYZES THE CLEAVAGE OF-5-OXO-L-PROLINE TO FORM L-
GLUTAMATE COUPLED TO THE HYDROLYSIS OF ATP TO ADP AND INORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by cDNA cloning.";
J. Biol. Chem. 271:32293-32300(1996).
                                                                                                                                                                                                           20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
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                                                                                                                                                                                                HUNTINGTIN INTERACTING PROTEIN 1 (HIP-I) (FRAGMENT)
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                         *Genomic organization of the human HIP1 gene and its candidate gene in a family diagnosed with Huntington
                                                                                                                                                                                                                                                                                                                                                                                   42 AGGTCATCAGGGTTGTAAGGCATCTCACATTTACAATACC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                86 CATGTGAAACTTACCAGTCAGTGCAGCCCT......CGCATTGCGCCCATT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMODIMER.
TISSUE SPECIFICITY: WELL EXPRESSED IN TESTIS, K
SIMILARITY: BELONGS TO THE OXOPROLINASE FAMILY.
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CATALYTIC ACTIVITY: ATP + 5-OXO-L-PROLINE + 2 H(2)O =
                                                                                                                                                                                                                                                                                                                                                     gGlyHisThrAlaCysAlaAspAlaTyrLeuThrProThr
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MEDLINE-20515263; PubMed-=11063258;

Chopra V.S., Metzler M., Rasper D.M., Engqvist-Goldstein A.E.Y.,

Singaraja R., Gan L., Fichter K.M., McCutcheon K., Drubin D.,

Nicholson D.W., Hayden M.R.;

"HIP12 is a non-proapoptotic member of a gene family including H

an interacting protein with huntingtin.";

Mamm. Genome 11:1006-1015/2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wanker E.E., Rovira C., Scherzinger E., Hasenbank Tait D., Colicelli J., Lehrach H.;
"HIP-I: a huntingtin interacting protein isolated hybrid system.";
                                                                             EMBL;
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Kalchman M.A., Kolde H.B., McCutcheon K., Graham R.K., Nichol K.
Nishiyama K., Kazemi-Esfarjani P., Lynn F.C., Wellington C.,
Nishiyama K., Kazemi-Esfarjani P., Lynn F.C., Wellington C.,
Metzler M., Goldberg Y.P., Kanazawa I., Geitz R.D., Hayden M.R.;
"HIP1, a human homologue of S. cerevisiae Sla2p, interacts with
membrane-associated huntingtin in the brain.";
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SEQUENCE OF 82-995 FROM MEDLINE-97285121; PubMec
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BY ALTERNATIVE SPLICING.
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                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE SLA2 FAMILY.
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 AF052270;
AF052271;
AF052272;
AF052273;
AF052274;
AF052274;
AF052275;
AF052275;
AF052277;
AF052277;
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AF052264;
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01-OCT-1989 (Rel. 1
20-AUG-2001 (Rel. 4
MICROSOMAL SIGNAL P
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CONFLICT
SEQUENCE
         "cDNA-derived primary structure of the glycoprotein canine microsomal signal peptidase complex.";
J. Biol. Chem. 263:17063-17070(1988).
-i- FUNCTION: MICROSOMAL SIGNAL PEPTIDASE IS A MEMBE
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SMART; SM00307; ILWEQ;
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                                                                      SEQUENCE FROM N.A.,
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AC004491; AAC08319
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40, Last annotation
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KLHSCLP -> SERAAAST (IN REF. 4
LMOLEE -> STRPRI (IN REF. 4).
W; 72BDAA16AFD15C40 CRC64;
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KDA SUBUNIT (EC 3.4.-.-) (SPC22/23).
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seq_name: SwissProt_39:MOBA_ECO57
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US-09-684-016-48411 x SPC2_CANFA
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CONFLICT
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STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last seq
20-AUG-2001 (Rel. 40, Last ann)
MOLYBDOPTERIN-GUANINE DINUCLEO
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                                                                                                                                                  Bacteria; Proteobacteria;
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SUBUNIT: COMP
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SUBCELLULAR LOCATION: TYPE II MEMBI
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DINUCLEOTIDE BIOSYNTHESIS PROTEIN
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CYTOPLASMIC (POTENTIAL)
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342AB8E0F3F6D71A CRC64;
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                                                                                                                                                   subdivision; Enterobacteriaceae;
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Identity: 42
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P32173; Q9LBV0;
01-OCT-1993 (Rel. 27, C
01-OCT-1993 (Rel. 27, C
20-AUG-2001 (Rel. 40, I
MOLYBDOPTERIN-GUANINE [
                                                                                                                                                       documentation_block:
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[3]
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 Escherichia
               Bacteria;
                           Escherichia
                                        MOBA OR MOB OR CHLB
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or send an email to license@isb-sib.ch).
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Kurokawa K., Yasunaga T., Makino K., Shinagawa
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DINUCLEOTIDE BIOSYNTHESIS
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H., Hayashi
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MEDLINE-93347969; PubMed-8346018;
MEDLINE-93347969; PubMed-8346018;
Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
Plunkett of the Escherichia coli genome. III. DNA sequence of the "Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.";
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MEDLINE=20568278; PubMed=10978347;
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"The crystal structure of the Escherichia coli MobA protein provides insight into molybdopterin guanine dinucleotide biosynthesis.";
J. Biol. Chem. 275:40211-40217(2000).
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SUBUNIT: MONOMER.
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COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY.
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1FR9; 10-JAN-01.
1FRW; 10-JAN-01.
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                                                                                        473 tAsnAsnAlaAspPheIleIleThrSerThrTyrGlnGluIleAlaGlyT
                                                                                                                                                                         457 GluAspLysTyrHisPheSerCysGlnPheThrAlaAspLeuIleAlaMe
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Buchner P., Poret M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; S
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SUCROSE SYNTHASE 2 (EC 2.4.1.13) (SUCROSE-U
                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUS2_PEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
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CATALYTIC ACTIVITY: UDP-GLUCOSE + D-FRUCTOSE = U
hr {\tt LysAsnThrIleGlyGlnTyrGluSerHisThrAlaPheThrLeuPro}
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                                                                                                                                                                                                                                                                       1/1
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                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
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                                            ......CAGCCCTCGCATTGCGCCATTAGGTCATCA
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2.4.1.13) (SUCROSE-UDP)
                                                                                                                                                                                                                                                                       from: 1
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STANDARD;

PRT;

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SwissProt\_39:FBP2\_STRPU

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   Quality:
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Percent Similarity:
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FBP2_ST
P15216;
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InterPro; IPR001881; I
Pfam; PF00008; EGF; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00022; EGF_1; FALSE_NEG. PROSITE; PS01186; EGF_2; 4.
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P04070; laut.
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N II PRECURSOR
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51.50
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14, Last sequence update;
33, Last annotation update;
33(EURSOR (EPIDERMAL GROWTH FACTOR-RELATED)
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Percent Identity: 64.286
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EGF-LIKE 2.
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EGF-LIKE 4.
BY SIMILARITY.
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MBL outstation -
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seq_name: SwissProt_39:HEX9_ADECC
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                                                                                                                                                                                                     Percent Similarity:
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                                                                                                                                                                                                                                                                                  Pfam; PF00628; PHD; 1.
Pfam; PF00856; SET; 1.
SMART; SM00249; PHD; 1.
SMART; SM00317; SET; 1.
PROSITE; PS50280; SET; 1.
Hypothetical protein; Zinc-finger.
SEQUENCE 859 AA; 94886 MW; B486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _documentation_block:
YDBB_SCHPO STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q10362;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 94.9 KDA PROTEIN C22E12.11C IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001965;
InterPro; IPR001214;
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 270043; CAA93898.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast)
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                          21 uSerCysGluValTrp 26
                                                                                                          11 AAATGTGAGATGCCTTACAACCCTGATGAC...CTAATGGCGCAATGCGA
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                                                    GGGCTGCACTGACTGG
                                                                               ArgCysValCysProPheGluAspAspAspGlyPheThrIleGlnCysGl
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Ratio:
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Gaps:
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US-09-684-016-48411 x HEX9_ADECC
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HEX9 ADECC STANDARD;
                                                                        DMSB_ECOLI STANDARD; PRT; 204 AA P18776; P77745; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation updat ANAEROBIC DIMETHYL SULFOXIDE REDUCTASE CHAIREDUCTASE IRON-SULFUR SUBUNIT).

DMSB OR B0895.
Escherichia coli.
Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morrison M.D., Onions D.E., Nicolson L.;
"Complete DNA sequence of canine adenovirus type 1.";
J. Gen. Virol. 78:873-878(1997).
-i- FUNCTION: THIS PROTEIN IS A STRUCTURAL COMPONENT OF THE VIRION.
MAY HAVE AN ADDITIONAL ROLE DURING ADENOVIRUS MULTIPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U55001;
EMBL; Y07760;
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Campbell J.B., Zhao Y.;
Submitted (AUG-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine adenovirus type 1 (strain CLL), Canine adenovirus type 1 (strain RI261) Viruses; dsDNA viruses, no RNA stage; ACBL_TaxID-69150, 69151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
HEXON-ASSOCIATED PROTEIN (PROTEIN IX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hexon-associated protein.
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CAA69055.1;
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PROSITE; PS0019
Oxidoreductase;

PS00198;

4FE4S\_FERREDOXIN;

Electron

transport;

4Fe-4S;

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EMBL; AE000191; AAC73981.1;
EMBL; D90727; BAA35627.1;
PIR; S03786; S03786.
HSSP; P00195; ICLF.
EcoGene; EG10233; dmsB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Ikimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
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InterPro; IPR001450; 4FE4S_ferrdxin.
Pfam; PF00037; fer4; 1.
                                                                                                                                        EMBL; J03412; AAA83844.1; -. EMBL; AE000191; AAC73981.1;
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A 718-kb DNA sequence of the corresponding to the 12.7-28.0 DNA Res. 3:137-155(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                MEMBRANE ANCHOR PROTEIN.
SIMILARITY: THE IRON-SULFUR CENTERS
'BACTERIAL-TYPE' 4FE-4S FERREDOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COFACTOR: IRON-SULFUR.
SUBUNIT: THE COMPLEX CONSIST OF THREE SUBUNITS:
REDUCTASE; DMSB, AN ELECTRON TRANSFER PROTEIN,
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US-09-684-016-48411 x DMSB_ECOLI
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                                                                                         complementation in Escherichia coli.";
J. Biol. Chem. 265:9011-9014(1990).
-i- CATALYTIC ACTIVITY: 1-(5-PHOSPHORIBOSYL)-4-(N-SUCCINO-CARBOXAMIDE)
-5-AMINOIMIDAZOLE = FUMARATE + 5'-PHOSPHORIBOSYL-5-AMINO-4-
IMIDAZOLECARBOXAMIDE (ALSO CATALYZES: N6-(1,2-DICARBOXYETHYL)AMP =
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Gallus gallus (Chicken).

Metazoa; Chordata;
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SEQUENCE
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01-MAY-1991 (Rel. 18, Last sequence update)
30-MAY-2090 (Rel. 39, Last annotation update)
ADENYLOSUCCINATE LYASE (EC 4.3.2.2) (ADENYLOSUCCINASE) (ASL) (ASASE)
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METAL
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MEDLINE=90264380; PubMed=2111814;
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                      SIMILARITY: BELONGS SUBFAMILY.
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PATHWAY: EIGHT STEP
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                                                                                                                                                                                  Dixon J.E.;
functional
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                                                                                                                                                                                                                                                                                                                            Phasianinae;
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alignment_scores:
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PRINTS; PRO0149; FUMRATELYASE.

PROSITE; PS00163; FUMRATELYASES; 1

Purine biosynthesis; Lyase.

ACT_SITE 134 134 BASE (B'SEQUENCE 459 AA; 51786 MW; E5EC1
                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
E315_ADE05 STANDARD;
MEDLINE-92148953; PubMed-1531370; Krajcsi P., Tollefson A.E., Anderson C.W., Wold W.S.M.; Krajcsi P., Tollefson A.E., Anderson C.W., which is required for "The adenovirus E3 14.5-kilodalton protein, which is required for down-regulation of the epidermal growth factor receptor and prevention of tumor necrosis factor cytolysis, is an integral membrane protein oriented with its C terminus in the cytoplasm."; J. Virol. 66:1665-1673(1992).
                                                                                                                                                             IDENTIFICATION OF PROTEIN.
MEDILINE-90177214; PubMed-2309441;
Tollefson A.E., Krajcsi P., Pursley
"A 14,500 MW protein is coded by rec
                                                                                                                                                                                                                              MEDLINE-85092388; PubMed-2981456; Cladaras C., Wold W.S.M.; "DNA sequence of the early E3 tra Virology 140:28-43(1985).
                                                                                                                                                                                                                                                                                                                         Human adenovirus type 5. Viruses; dsDNA viruses, no
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01-JAN-1988 (Rel. 06, Last
20-AUG-2001 (Rel. 40, Last
EARLY E3B 14.6 KDA PROTEIN
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                                                                                                            SIGNAL SEQUENCE CLEAVAGE SITE
                                                                                                                                                  "A 14,500 MW protein adenoviruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                                     Virology 175:19-29(1990)
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BASE (BY SIMILARITY).
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seq_documentation_block:
ID SPC2_CHICK STAN
AC P28687;
DT 01-DEC-1992 (Rel. 2
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P28687;
01-DEC-1992 (Rel.
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"The E3-14-5K integral membrane protein of adenovirus that is required for down-regulation of the EGF receptor and for prevention of TNF cytolysis is 0-qlycosylated but not N-glycosylated.";
Virology 188:570-579(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The sequence of the genome of adenovirus type 5 and its
with the genome of adenovirus type 2.";
Virology 186:280-285(1992).
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SIMILARITY: TO EQUIVALENT PROTEIN IN OTHER ADENOVIRUSES.
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X03002; CAA26786.1; -.
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fson A.E., Wold W.S.M.;
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01-AUG-1988 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBUNIT: HEN OVIDUCT SIGNAL PEPTIDASE ACTIVITY IS ASSOCIATED WITH AN APPARENT COMPLEX OF ONLY TWO PROTEINS, WITH ESTIMATED MOLECULAR MASSES OF 19 AND 23 KDA.

-i- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MICROSOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning of a cDNA encoding microsomal signal peptidase."; Biochem. J. 282:447-452(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92189580; PubMed=1546959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
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                                                                                                                                                        AspTleThrAlaAspLeuGlnSerIlePheAspTrpAsnValLysGlnLe
                                                                                                 uPheLeuTyrLeuSerAlaGluTyrSerThrLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MICROSOMAL. SIMILARITY: TO OTHER VERTEBRATES SPC22/23 AND TO YEAST SPC3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: MICROSOMAL SIGNAL PEPTIDASE IS A MEMBRANE-BOUND ENDOPROTEINASE THAT REMOVES SIGNAL PEPTIDES FROM NASCENT
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                                                                       SwissProt_39:NGFR_HUMAN
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S22412; S22412.
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1 32
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                             STANDARD;
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71.429
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36, Last annotation update)
PEPTIDASE 23 KDA SUBUNIT (EC
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164
141
20230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.W.,
 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsome; Endoplasmic reti
Signal-anchor.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .'
                                                                                                                                                                                                                                                                                                                                                                    MW.
                                                                                                                                                                                                                                                                                   Percent
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                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .).
; A5572439EB8210AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             HYDROPHOBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL-ANCHOR (TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasiani
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                                                                                                                                                                                                                                                                                    Identity:
                                                                                                                                                                                                                                                                                               Length:
Gaps:
                                                                                                                                                                                                                to:
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                              427
                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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39.286
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01-AUG-1988 (Rel. 0)
20-AUG-2001 (Rel. 4)
LOW-AFFINITY NERVE
(GP80-LNGFR) (P75 II
NGFR OR TNFRSF16.
  DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                          REPEAT
REPEAT
                                                                                                DOMAIN
REPEAT
REPEAT
                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                             Pfam; PF00531; death; 1.

Pfam; PF00020; TNFR_c6; 4.

SMART; SM00005; DEATH; 1.

SMART; SM00208; TNFR; 3.

PROSITE; PS00652; TNFR_NGFR_1; 3.

PROSITE; PS50050; TNFR_NGFR_2; 4.

PROSITE; PS50017; DEATH_DOMAIN; 1.

Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     EMBL; M14764; AAB59544.1; -.
EMBL; M21621; AAA36363.1; -.
PIR; A25218; GQHUN.
HSSP; P07174; INGR.
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                                                                                                                                                            DOMAIN
                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                   InterPro; IPR000488;
InterPro; IPR001368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor gene.";
Mol. Cell. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89096903; PubMed=2850
Sehgal A., Patil N., Chao M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Expression and structure of the human NGF receptor."; Cell 47:545-554(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-87051725; PubMed-3022937;
MEDLINE-87051725; PubMed-3022937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                          Phosphorylation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson D., Lanahan A
Bothwell M., Chao M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                           MIM; 162010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A constitutive promoter directs expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-22 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
SIMILARITY: CONTAINS A LA-NGER/TWPE CYSTEINE-RICH REGI
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND NT-3, AND NT-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NT-3, AND NT-4.
SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOND FORMATION.
   29
251
273
31
31
108
148
344
344
47
67
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PubMed=2850481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08, Last sequence update)
40, Last annotation update)
GROWTH FACTOR RECEPTOR PRECURSOR
   250
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427
189
189
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64
                                                                                                                                                                                                                                                                                                               TNFR_c6
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4 X TNER-CYS.
TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 3.
TNER-CYS 4.
DEATH.
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                                               EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                  LOW-AFFINITY NERVE GROWTH FACTOR
  Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
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alignment_scores:
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Ratio:
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US-09-684-016-48411 x NGFR_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              documentation_block:
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
STRAIN-NIH SWISS;
Train-NIH SWISS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
DISULFID
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DISULFID
                                                                                                                                                        "Tctex3, related to Drosophila polycomblike, cells and mapped to the mouse t-complex."; Mamm. Genome 9:874-880(1998).
                                                                                                                                                                                           MEDLINE-99018220; PubMed-9799836;
Kawakami S., Mitsunaga K., Kikuti Y.Y., Ando A., Inoko H.,
Yamamura K., Abe K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHD FINGER PROTEIN 1 (PHF1 PROTEIN) (T-COMPLEX TESTIS-EXPRESSED
                                                                                                                -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
-!- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123
                                                                                                                                                                                                                                      TISSUE=Testis
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                       (POLYCOMBLIKE 1) (MPCL1).
PHF1 OR TCTEX3 OR TCTEX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9Z1B8; O54808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHF1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 CysArgCysAlaTyrGlyTyrTyrGlnAspGluThrThrGlyArgCysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 GGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uAlaCys
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                                                                                                                                                                                                                                                                           (DEC-1996)
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427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
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Rodentia;
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SER/THR-RICH.
SER/THR-RICH.
V-LINKED (GLCNAC. . .) (POT
                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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to:
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                                                                                                                                                                                                                                                                                                  S.M.;
interacts with polycomb-group
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36.842
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; Murinae; Mus
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InterPro; IPR00299; Tudor.
Pfam; PM0028; PHD; 2.
SMART; SM00249; PHD; 2.
SMART; SM0033; TUDOR; 1.
CONFLICT 89 142 PH
ZN_FING 188 237 PH
ZN_FING 188 237 PH
CONFLICT 249 249 L
CONFLICT 377 377 R
CONFLICT 377 377 R
CONFLICT 558 559 G
CONFLICT 558 559 IF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

Mashreghi-Mohammadi M.;

Mashreghi-Mohammadi M.;

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases

-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PHF1 AND 2/PHF2

-RE PRODUCED BY ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: HIGHEST LEVELS IN HEART, SKELET, PANCREAS, LOWER LEVELS IN BRAIN, PLACENTA, LUNG, LIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHD FINGER PROTEIN 1 (PHF1 PROTEIN).
                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
Wang J.H., Du G.W., Zhou Y., Yuan J.G., Qiang
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=98207256; PubMed=9545646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHF1_HUMAN
O43189; O60929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                               Genomics
                                                                                                                                                                                                                                                                                                                                                                                           similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                Coulson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 sArgSerCysLeuGlnTrp 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188
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                                                                                                                                                                                                                                                                                                                                                       son M., Robert S., Eyre H.J., Saint I identification and localization of a larity to Polycomblike of Drosophila nics 48:381-383(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SwissProt_39:PHF1_HUMAN
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PHD-TYPE 1.
PHD-TYPE 2.
L -> F (IN REF. 1).
G -> E (IN REF. 2).
R -> S (IN REF. 2).
G -> R (IN REF. 2).
IF -> HLPDSLLLLDSPFTHWHFHAI 2).
M; 6D2EE5F53D6164C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Identity:
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E (IN REF. 2).
S (IN REF. 2).
R (IN REF. 2).
HLPDSLLLLPSPFTHWHFHALDL (IN REF
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a human gene with sequence
la melanogaster.";
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: 39.130
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databases.
                                                                                        2/PHF2 (SHOWN HERE);
                                    SKELETAL MUSCLE,
             LIVER,
             AND
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seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00628; PHD; 2.
SMART; SM00249; PHD; 2.
SMART; SM00333; TUDOR; 1.
SMART; SW00333; TUDOR; 1.
SMART; SW00333; TUDOR; 1.
SMART; SW00333; TUDOR; 1.
SMART; SW0033; TUDOR; T
                        Scanlan M.J.,
Jongeneel V.,
Old L.J.;
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SEQUENCE
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EMBL;
                                                                                         SEQUENCE FROM N.A.
MEDLINE=99438124; PubMed=10508479;
                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                           20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
BS4 PROTEIN (NY-REN-18 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                          BS4_HUMAN
Q9Y5A7; 095422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                       NYREN18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 sArgSerCysLeuGlnTrp 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 TyrCysTyrCysGlyGlyProGlyGluTrpAsnLeuLysMetLeuGlnCy
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                                                 Gordan J.D., Williamson Gure A.O., Jager D., Jag
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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    autologous
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SFPSGOGPGGGVSRPLGKRRRPEPEPLRRRQKGKVEELGPP
SAVRNQPEPQEQRERAHLQRALQASVSPPSPSPNQSYQGSS
GYNERPTDARCLPSSPIRMFASFHPS -> RAGPWGRGLTS
PGEAPEAGARAPEEEAEGESGGAGATLSSAQSARAPGAEGA
GSSAEGTAAAPSGCLLPSTLLPAPQGPLGTVDPQTGHPWNF
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MISSING (IN ISOFORM 1).
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                                                 Jager E.,
    antibody
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Gaps:
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E., Knuth
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                                                 Bander N.H.
Chen Y.-T.,
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seq_name: SwissProt_39:SUSY_BETVU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: BS4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-684-016-48411/rev x BS4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
SUCROSE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
                                                                                               Beta vulgaris (Sugar beet).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
                                                                                                                                                                                                                                                                                                                                                                                    SUSY_BETVU
Q42652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401
TISSUE=Tap root;
                         SEQUENCE FROM N.A.
                                                                             NCBI_TaxID=3555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000449; UB
Pfam; PF00627; UBA; 2.
SMART; SM00165; UBA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Korenberg J.;
Submitted (NOV-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases -! SIMILARITY: CONTAINS 3 UBA DOMAINS.
                                                                                                                                                                                                                                                  (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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Int. J. Cancer 83:456-464(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spGlyAsnValAspHisAlaAlaThrHisIleThrAsn 413
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601
                                                                                                                                                                                                                                                                      (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
THASE (EC 2.4.1.13) (SUCROSE-UDP G
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UBA 2.
UBA 3.
D -> DNYRTTGIATIEVFLPPRLKKDLAKQYSDRLECCEN
EVEKVIEEIRCKAIERGTGND (IN REF. 2).
R -> K (IN REF. 2).
p5a6eCae0B3a975B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                         GLUCOSYLTRANSFERASE)
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seq_name: SwissProt_39:BAR3_CHITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                              Q03376;
Q1-OCT-1993 (Rel. 27, C
Q1-OCT-1993 (Rel. 27, I
Q1-OCT-1994 (Rel. 30, I
BALBIANI RING PROTEIN 3
                                                                                                                                                                                                                                               documentation_block:
                                                                                                                                                                                                                                                                                                                449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Mol. Biol. 30:863-872(1996).

-i- FUNCTION: SUCROSE-CLEAVING ENZYME THAT PROVIDES UDP-GLUCOSE A FRUCTOSE FOR VARIOUS METABOLIC PATHWAYS.

-i- CATALYTIC ACTIVITY: UDP-GLUCOSE + D-FRUCTOSE = UDP + SUCROSE.

-i- TISSUE SPECIFICITY: EXPRESSED MOST PREDOMINANTLY IN TAP ROOT.
                                                                                               Eukaryota;
                                                                                                                Chironomus tentans (Midge)
                                                                                                                                                                                                                                                                                                                                                                                                                                            415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001296; Glycos_transf_1.
InterPro; IPR000368; Sucrose_synth.
Pfam; PP00534; Glycos_transf_1; 1.
Pfam; PP00862; Sucrose_synth; 1.
TISSUE=Salivary gland;
                 SEQUENCE FROM N.A
                                                 NCBI_TaxID=7153;
                                                                    Chironomoidea;
                                                                                 Pterygota;
                                                                                                                                                                                                                                  BAR3_CHITE
                                                                                                                                                                                                                                                                                                                                                                             432 hrLysAsnThrValGlyGlnTyrGluSerHisLysAlaPheThrPhePro 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 GAAGATAAGTATCACCTTACATGTGAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X81974; CAA57499.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Expression analysis of a sucrose
vulgaris L.).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96270366; PubMed=8639746; Hesse H., Willmitzer L.;
                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                               GGGTTGTAAGGCATCTCACAT 13
                                                                                                                                                                                                                                                                                                              GlyLeuTyrArgValValHis 455
                                                                                                                                                                                                                                                                                                                                                                                                                                           tAsnHisAlaAspPheIleIleThrSerThrTyrGlnGluIleAlaGlyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: TO OTHER PLANTS SUCROSE SYNTHASE.
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Ratio:
                                                              Metazoa; Arthropoda; Tracheata; Hexapoda; I
Neoptera; Endopterygota; Diptera; Nematoces
dea; Chironomidae; Chironominae; Chironomus
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                                                                                                                                                                                                                                  STANDARD;
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2.273
38.596
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                                                                                                                                                               Last sequence update)
Last annotation updat
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Identity:
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2
26.316
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                                                                                                  Insecta;
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AC OCC OCC RR R R A A R A A
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                                                                                                                                                                                                                                                                                          RBB2_HUMAN
P2375;
01-DEC-1992 (Rel. 24, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-7001 (Rel. 40, PROTEIN 2 (RBBP-2).
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Paulsson G., Lendahl U., Galli J., Ericsson C., Wieslander L.;
Paulsson G., Lendahl U., Galli J., Ericsson C., Wieslander L.;
Paulsson G., Lendahl U., Galli J., Ericsson C., Wieslander L.;
"The Babblani ring 3 gene in Chironomus tentans has a diverged repetitive structure split by many introns.";
J. Mol. Biol. 211:331-349(1990).
J. Mol. Biol. 211:331-349(1990)
                                            SEQUENCE FROM N.A.

MEDLINE-94020841; PubMed-8414517;

Fattaey A.R., Helin K., Dembski M.S., Dyson N.,

Vuocolo G.A., Hanobik M.G., Haskell K.M., Oliff
Jones R.E.;
                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Interpro
"Characterization RBP2.";
                                                                                                                                                                                             NCBI_TaxID=9606;
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PRINTS; PR00876; MTNEMATODE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oGlyGlyGlnAspTrp 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysGlnCysGluCysPro.....LysAspLysProLysLysGlnCysPr 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
Similarity:
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DOMAIN: HAS 82 APPROXIMATE REPEATS OF CYS-X-CYS-X-CYS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; x52263; CAA36506.1;
S08167; S08167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SwissProt_39:RBB2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
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AA; 186145
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                       the retinoblastoma
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                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identity:
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to:
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                    binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
1
45.455
                                                                   Harlow
A., Def
                    proteins RBP1
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                                                                     Defeo-Jones
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Seq. ID AC DT DT DT DT DT OC
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US-09-684-016-48411 x RBB2_HUMAN
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    Quality:
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Pfam; PF00275; jmjN; 1.

R Pfam; PF00628; PHD; 3.

R SMART; SM00501; BRIGHT; 1.

SMART; SM00545; JmjN; 1.

SMART; SM00249; PHD.

Trans-actino f
                                                                                                                                                                                                                                                                                     Align seg
                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                 1176
                                                                                                                _documentation_block:
COBJ_PSEDE STANDARD;
                                                                                                                                                                                                                                 1162 LysPheCysIleCysArgLys.....ThrAlaSerGlyPheMetLeuGl 1176
                                               01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PRECORRIN-3B C17-METHYLTRANSFERASE (EC 2.1.1.131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
Pfam; PF01
                            СОВЛ
                                                                                                     COBJ_PSEDE
P21640;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Defeo-Jones D., Huang P.S., Jones R.E., Hanobik M.G., Huber H.E., Oliff A.; "Cloning of cDNAs for cellular proteins retinoblastoma gene product."; Nature 352:251-254(1991).
             Pseudomonas
                                       METHYLTRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S66431; AAB28544.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1102-1569 FROM N.A. MEDLINE=91312450; PubMed=1857421;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                             52 ATGCGAGGGCTGCACTGACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                               nCysGluLeuCysLysAspTrp 1183
                                                                                                                                                                                                                                                             AGGTATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
SIMILARITY: TO THE C-TERMINAL DOMAIN OF THE XE169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE JUMONJI PROTEIN.
                                                                                                                                                      SwissProt_39:COBJ_PSEDE
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IPR003349;
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1722 AA;
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             denitrificans
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19; PHD; 3.
factor; Nuclear protein.
MISSING (IN REF. 2).
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3.333
62.500
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JmjC.
JmjN.
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                                                                                                                   PRT;
                                        METHYLASE)
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                                                                                                                   254
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                                                                                                                   AA
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                                                                                                                                                                                                                                                                                                                                                                      24
                                                   (PRECORRIN-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
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Bacteria;

Proteobacteria;

gamma subdivision; Pseudomonadaceae;

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seq_documentation_block:
ID CAIF_HUMAN STANDA
AC Q07092;
DT 01-FEB-1995 (Rel. 31,
DT 01-FEB-1995 (Rel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-016-48411/rev x COBJ_PSEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crouzet J., Cameron B., Cauchois L., Rigault S., Rouyez M.-C. Blanche F., Thibaut D., Debussche L.; "Genetic and sequence analysis of a 8.7-kilobase Pseudomonas denitrificans fragment carrying eight genes involved in transformation of precorrin-2 to cobyrinic acid."; "Bacteriol. 172:5980-5990(1990).
                                                                                                                                                                                                                                                                                                                                                                                              119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00590; TP_methylase; 1. Cobalamin biosynthesis; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; E36145; E36145.
InterPro; IPR000878; Corrin_porph_mthyltrnf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94042919; PubMed=8226690; Debussche L., Thibaut D., Cameron B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {	t Methyltransferase.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M59301; AAA25798.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas.
NCBI_TaxID=43306;
                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 175:7430-7440(1993).
- FUNCTION: METHYLTRANSFERASE THAT CATALYZES THE METHYLATION
- C-17 IN PRECORRIN-3B TO FORM PRECORRIN-4.
- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + PRECORRIN-3B
ADENOSYL-L-HOMOCYSTEINE + PRECORRIN 4.
                                                                                                                                                                                                                                                                                                                                                                                       aValAlaAlaArgTleGlyAlaProLeuGlyHisAspPheCysAlaIleS
                                                                                                                                                                                                                                                                  er
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGCAGCCCTCGCATT...GCGCCATTAGGTCATCAGGGTTGTAAGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TrpLysSerValGluLeuValIleThrProGlyValThrAlaMetLeuAl
                                                                                                                                                                                           SwissProt_39:CA1F_HUMAN
                                                                                                                                                                                                                                                                  136
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(Rel. 31, Created)
(Rel. 31, Last sequence update)
                                                                                                    STANDARD;
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2.475
58.824
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Gaps: 1
Identity: 38.235
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e of coenzyme
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ne B12 in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO OTHER
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Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QF
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                               Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S23810; S23810. MIM; 120326; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01391; Collagen; 16. Pfam; PF02210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cysteine-containing non-collagenous J. Biochem. 112:856-863(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000087; Colle
InterPro; IPR003129; TSPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>:</del>
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COLLAGEN ALPHA 1(XVI)
                                                                             DOMAIN
                                                                                                   DOMAIN
                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                  Extracellular matrix; Connective tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kanamori T., Yamakoshi H., Nagai Y.;
"Molecular cloning and partial characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamaguchi N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93203161; PubMed=1284248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc.
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Pan T.C., Zhang R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 418-1603 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILINE-92335339; PubMed-1631157;
MEDILINE-92335339; PubMed-1631157;
MEDILINE-92355339; PubMed-1631157;
MEDILINE-92355339; PubMed-1631157;
MEDILINE-92355339; PubMed-1631157;
MEDILINE-92355339; PubMed-1631157;
MEDILINE-92355339; PubMed-1631157;
MEDILINE-92355339; PubMed-1631157;
MEDILINE-9235339; PubMed-1631157;
MEDILINE-9235339; PubMed-1631157;
MEDILINE-9235339; PubMed-1631157;
MEDILINE-9235339; PubMed-1631157;
MEDILINE-9235339; PubMed-1631157;
MEDILINE-9233539; PubMed-1631157;
MEDILINE-9235539; PubMed-1631157;
MEDILINE-9235539; PubMed-1631157;
MEDILINE-923559; PubMed-1631157;
MEDILINE-92359; PubMed-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WITH OTHER TYPES OF COLLAGEN.

DEVELOPMENTAL STAGE: TRANSLENTLY ELEVATED EXPRESSION DURING
GESTATION, AND DECREASE AT TERM.

DOMAIN: THIS SEQUENCE DEFINES EIGHTEEN DIFFERENT DOMAINS, NINE
TRIPLE-HELICAL DOMAINS (COL9 TO COL1) AND TEN NONTRIPLE-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
SIMILARITY: BELONGS TO THE FAMILY OF FIBRIL-ASSOCIATED COLLAGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAINS (NC10 TO NC1).
PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMNION, IT IS FOUND IN AN ACELLULAR, RELATIVELY DENSE LAYER OF A COMPLEX NETWORK OF RETICULAR FIBERS. ALSO LOCATED TO A FIBROBLAST LAYER BENEATH THIS DENSE LAYER. EXISTS IN TISSUES IN ASSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THE NUMEROUS INTERRUPTIONS IN THE TRIPLE HELIX MAY MAKE THIS MOLECULE EITHER ELASTIC OR FLEXIBLE. TISSUE SPECIFICITY: IN THE PLACENTA, WHERE IT IS FOUND IN THE AMNION, A MEMBRANOUS TISSUE LINING THE AMNIOTIC CAVITY WITHIN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M92642; AAA58427.1;
S57132; AAB25797.1;
                                                                                                                                                                                                                                                                                                            Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha 1(XVI), consisting of repetitive collagenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERRUPTED HELICES (FACIT)
                                                                           555
572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Kimura S., McBride O.W., Hori H.,
Yamakoshi H., Nagai Y.;
                                                                                                                                                                                                                                                                                                                                                                                          TSPN;
                                                                                                                                                                                                                              21
1603
374
505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last annotation update) CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .' .'
                                                  WITH 1
                                                                           TRIPLE-HELICAL REGION 7
                                                                                                   WITH 1 IMPERFECTIC NONHELICAL REGION
                                                                                                                                                      TRIPLE-HELICAL REGION
                                                                                                                                                                              NONHELICAL REGION 9
                                                                                                                                                                                                      TRIPLE-HELICAL REGION 9 (COL9) WITH 3 IMPERFECTIONS.
                                                                                                                                                                                                                                                         COLLAGEN ALPHA 1(XVI) CHAIN. NONHELICAL REGION 10 (NC10).
  TRIPLE-HELICAL REGION 6 (COL6)
                          NONHELICAL REGION 7 (NC7)
                                                                                                                              IMPERFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          segments.";
                                                     IMPERFECTION.
                                                                                                                                                                                                                                                                                                                                                            Collagen; Hydroxylation;
                                                                                                        æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a novel collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada Y.,
                                                                                                        (NC8)
                                                                                                                                                                                 (NC9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NONTRIPLE-HELICAL
                                                                                                                                                      8 (COL8)
                                                                           (COL7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domains
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Sequence of the control of the contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
      Rasmussen S.W;
Rasmussen S.W;
"A 37.5 kb region of yeast chromosome and CSD3 genes, a TCP-l-related gene, and CSD3 genes, a TCP-lated gene, and tRNA(Arg).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 63.9 KDA PROTEIN IN IMEZ-MEF2 IN
                                                                                                                                                                                                                                                                                                                                                                                                       documentation_block:
  to the
Yeast 1
                                                                                             SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
MEDLINE-96090136; Pubm
                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
                                                                                                                                                                                                   Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                              YJL105W OR J0819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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11:873-883(1995).
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1.768
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WITH 2 IMPEREECTIONS
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WITH 2 IMPERFECTIONS.
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NONHELICAL REGION 1 (NC1).
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NONHELICAL REGION 6 (NC6)
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> P (IN REF. 2).
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E27D9A1D4E598A37 CRC64;
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                                                        X includes the SME1, MEF2,
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                                                                                                                                                                                                                                                                                 013724;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MANNOSYL-OLIGOSACCHARIDE GLUCOSIDASE (EC 3.2.1.106) (PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                               179
    Kalz-Fueller B., Bieberich E., Bause E.;
Eur. J. Biochem. 249:912-912(1997).
-i- FUNCTION: CLEAVES THE DISTAL ALPHA 1,2-LINKED GLUCOSE RESIDUE FROM
THE GLC(3)MAN(9)GLCNAC(2) OLIGOSACCHARIDE PRECURSOR HIGHLY
SPECIFICALLY.
                                                                                                  Kalz-Fueller B., Bieberich E., Bause E "Cloning and expression of glucosidase "Cur. J. Biochem. 231:344-351(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 CysIleCysGlySerSerAspSerLysAspGluLeuPheIleGlnCysAs 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical SEQUENCE 56
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Pfam; PF00856; SET; 1.
SMART; SM00249; PHD; 1
SMART; SM00317; SET; 1
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-i- SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
-i- SIMILARITY: CONTAINS 1 SET DOMAIN.
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560 AA; 63855 MW; 9A
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; YJL105W.
~1965; PHD.
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4.083
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Homo.
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alignment_block:
US-09-684-016-48411/rev
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                                                                                                                                                                                                                                                                                  documentation_block:
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CARBOHYD
SEQUENCE
MEDLINE=99156862; PubMed=10036191;
Rehli M., Den Elzen N., Cassady A.I., Ostrowski M.C., Hume D.A.;
"Cloning and characterization of the murine genes for bHLH-ZIP
transcription factors TFEC and TFEB reveal a common gene organiz,
for all MiT subfamily members.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                               TFEB OR TCFEB.
                                                                                                                                                                                              TRANSCRIPTION FACTOR EB.
                                                                                                                                                                                                                                                        Q9R210;
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                                                                            STRAIN=BALB/C;
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                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: FIRST ENZYME IN THE N-LINKED OLIGOSACCHARIDE PROCESSING PATHWAY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuAlaTrpTyrArgAlaArgArgAlaValThrLeuHisSerAlaProPr
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91840
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Rodentia;
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                                                                                                                                                                                                                                                                      475 AA.
                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
DR (TYPE-II
                                                                                                                                   Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
1
1.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
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RC
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                                                                                                                                                                                                                                 seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                      documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 56:111-120(1999).

-I- FUNCTION: PROBABLE TRANSCRIPTION FACTOR BINDS TO THE USF/MLTF SITIAND PROBABLY RECOGNIZES E-BOX SEQUENCES IN THE HEAVY-CHAIN IMMUNOGLOBULIN ENHANCER (BY SIMILARITY).

-I- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
SEQUENCE FROM N.A., TISSUE=Ovary;
                                                                                               'GLYCOPROTEIN ZP2) (ZONA PELLUCIDA ZP2 OR ZP-2.
                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ZONA PELLUCIDA SPERM-BINDING PROTEIN 2 PRECURSOR (ZONA PELLUCIDA
                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - -
                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00038; HELIX_LOOP_HELIX; 1. Transcription regulation; DNA-binding; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF079095; AAD20979.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                       NCBI_TaxID=10090;
                                                                               Mus musculus
                                                                                                                                                                                P20239;
                                                                                                                                                                                           ZP2_MOUSE
                                                                                                                                                                                                                                                                                                                  106 HisValSer...ProAlaGlnGlySerProLysProAlaProAlaAlaSe 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:103270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001092;
                                                                                                                                                                                                                                                                                       36 TCAGGGTTGTAAGGCATCTCACATTTACAATACC
                                                                                                                                                                                                                                                                                                                                             86 CATGTGAAACTTACCAGTCAGTGCAGCCCTCGCATTGCGCCATTAGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BHLH PROTEIN (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                                                                                                                                                                                                                                                              rProGlyValArgAlaGlyHisValLeuSerThr 132
                                                                                                                                                                                                                                   SwissProt_39:ZP2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
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•
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
248
297
363
                                                                                (Mouse)
                                                                                                                                                                                                                                                                                                                                                                          TFEB_MOUSE
                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                           48.50
2.553
67.857
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288
318
413
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                                                       Chordata;
Rodentia;
               AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLH_Myc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLH_dim.
               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 28
Gaps: 1
Percent Identity: 39.286
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LEUCINE-ZIPPER (POTENTIAL).
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
BASIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLN-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRONG TRANSCRIPTION ACTIVATION
                                                     Sciurognathi;
                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4249C6F501968326 CRC64
               OF.
                                                                                                              PROTEIN
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               35-50 AND
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(See http://www.isb-sib.
                                                                                                                                                                                                                                                                                         w
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                                                                                                           A
                                                       Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions on
                                                                                                                                                                                                                                                                                                                                               37
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375 alTyrSerHisGln 379

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alignment_block:
US-09-684-016-48411
                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                 Quality:
Ratio:
Percent Similarity:
                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A34782; A34782.
MGD; MGI:99214; Zp2.
InterPro; IPR001507; zona_pellucida.
Pfam; PF00100; zona_pellucida; 1.
PRINTS; PR00023; ZPELLUCIDA.
SMART; SM00241; ZP; 1.
 108
                                                                        353
                                                                                                                                                                                                                                                                                                                                 CARBOHYD
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                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M34148; AAA40586.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liang L.-F., Chamow S.M., Dean J.; "Occyte-specific expression of mouse of the zona pellucida genes."; Mol. Cell. Biol. 10:1507-1515(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90205829; PubMed=1690843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content if the and this statement is not removed. Usage by and
TTTATTCCACACAA 12:
                                               GGGCTGCACTGACTGGTAAGTTTCACATGTAAGGTGATACTTATCTTCAA 107
                                                                       CysHisCysGluSerProValSerIleAspGluLeuCysAlaGln...As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: EXPRESSED DURING THE 2-WEEK GROWTH PHASE OCGENESIS, PRIOR TO OVULATION.

PTM: PROTEOLYTICALLY CLEAVED AFTER FERTILIZATION, AND THIS MODIFICATION, ALONG WITH PRESUMED CHANGES IN ZP3 MAY PLAY AN IMPORTANT ROLE IN THE POSTFERTILIZATION BLOCK TO POLYSPERMY.

PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES
                        pGlyPheMetAspPhe..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP ZP2 ACTS AS A SECONDARY SPERM RECEPTOR.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRACELLULAR
                                                                                              TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 ZP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell. Biol. 10:1507-1515(1990). FUNCTION: ZP2 FORMS WITH ZP1 AND ZP3 THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00682;
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6
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                                                                                                                                                                                                                                                                        35
684
704
363
363
172
184
184
217
2017
                                                                                                                                                                                                                                                                                                                                                                                                                              582; ZP_DOMAIN; 1.
Signal; Sulfation;
                                                                                                                                                                                                                                                           AA;
                                                                                                                        ZP2_MOUSE
                                                                                                                                               x ZP2_MOUSE
                                                                                                                                                                                 48.50
2.553
50.000
                                                                                                                                                                                                                                                                        34
713
683
703
713
630
630
172
184
217
264
                                                                                                                                                                                                                                                           80209
                                                                                                                        from: 1
                                                                                                                                                                                                                                                           MW.
                                                                                                                                                                                    Percent
                                                                                                                                                                                                                                                                      N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                 ZP.
N-LINKED
                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                             ZONA PELLUCIDA SPERM-BINDING
                                                                                                                                                                                                                                                           DCF9AE6CCD3461EF
                                                                                                                                                                                                                                                                                                                                                                                                                                Sperm; Receptor; Transmembrane;
                                                                                                                                                                                Length: 38
Gaps: 2
Identity: ·34.211
                                                                                                                        6
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                                                                                                                                                                                                                                                                                                       (GLCNAC. .
                                                                                                                                                                                                                                                                                              (GLCNAC.
                                                                                                                         713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE 2-WEEK GROWTH PHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZONA PELLUCIDA,
S CROSS-LINKED E
                                                                                                                                                                                                                                                           CRC64;
                       .GluV
                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                    (POTENTIAL)
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                                                                       368
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                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN
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Seq_documentation_block:
ID P32592;
DT 01-CCT-1993 (Rel. 27,
DT 01-CCT-1993 (Rel. 27,
DT 01-CCT-1993 (Rel. 27,
DT 01-CCT-1993 (Rel. 27,
DT 20-AUG-2001 (Rel. 40,
DE INTEGRIN BETA-2 PRECE
DE 101-CCT-1993;
GN 17GB2 OR CD18.

OS BOS TAUTUS (BOVINE).
OC MAMMMAIIA; Eutheria; (OC MAMMMAIIA; Eutheria; (OC MAMMMAIIA; Eutheria; (OC MAMMMAIIA; Eutheria; (I)
RN 161 (I)
RN MEDLINE-92290287; Pul
RN SEQUENCE FROM N.A.
RX MEDLINE-93028437; Pul
Shuster D.E., Boswort
RT SEQUENCE FROM SELECTION:
RN MEDLINE-93028437; Pul
RN SEDUINE-93028437; Pul
RN SHUSTER D.E., Kehrili
RT "Identification and i
leukocyte adhesion da
RE ILENCOCYTE ACHES WITH
RN SHUSTER D.E. Kehrili
RT "IGENTIFICAN" (LAD)
RN SCOTATES WITH
AND FOR FIRRINOG
CC -1- SUBGLIULAR LOCA
CC -1- SUBGUNIT: HETEROD
CC SEQUENCE G-P-R I
CC DASSOCTATES WITH
CC LOMBETA-2 IS A RE
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CC DAMONG THE MOST C
CC AMONG THE MOST C
CC AMONG THE MOST C
CC DAMONG THE
           PRINTS; PR01186; INTEGRINB. ProDom; PD001811; Integrin_SMART; SM00187; INB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shuster D.E., Kehrli M.E. Jr., Ackermann M.R., Gilbert R.O.;
Shuster D.E., Kehrli M.E. Jr., Ackermann M.R., Gilbert R.O.;

"Identification and prevalence of a genetic defect that causes
leukocyte adhesion deficiency in Holstein cattle.";

Proc. Natl. Acad. Sci. U.S.A. 89:9225-9229(1992).

-i- FUNCTION: INTEGRIN ALPHA-L/BETA-2 IS A RECEPTOR FOR ICAM1, ICAM2,
ICAM3 AND ICAM4. INTEGRINS ALPHA-M/BETA-2 AND ALPHA-X/BETA-2 ARE
RECEPTORS FOR THE IC3B FRACMENT OF THE THIRD COMPLEMENT COMPONENT
AND FOR FIBRINGGEN. INTEGRIN ALPHA-X/BETA 2 RECOGNIZES THE
SEQUENCE G-P-R IN FIBRINGEN ALPHA-CHAIN. INTEGRIN ALPHA-M/BETA-2
REGOGNIZES P1 AND P2 PEPTIDES OF FIBRINGEN GAMMA CHAIN. INTEGRIN
ALPHA-M/BETA-2 IS ALSO A RECEPTOR FOR FACTOR X. INTEGRIN ALPHA-
D/BETA-2 IS A RECEPTOR FOR ICAM3 AND VCAM1.

-i- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-2

-i- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shuster D.E., Bosworth B.T., Kehrli M.
"Sequence of the bovine CD18-encoding
and murine glycoproteins.";
Gene 114:267-271(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92290287; PubMed=1351021;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
10-AUG-2001 (Rel. 40, Last annotation update)
INTEGRIN BETA-2 PRECURSOR (CELL SURFACE ADHESION GLYCOPROTEINS LFA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93028437; PubMed=1384046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSOCIATES WITH EITHER ALPHA-L, ALPHA-M, ALPHA-X OR ALPHA-D. SUBCELLULAR LOCARION: TYPE I MEMBRANE PROTEIN.

DISBASE: DEFECTS IN ITGB2 ARE THE CAUSE OF LEUKOCYTE ADHESION DEFICIENCY (LAD). THE MUTATION CAUSING LAD (GLY-128) IS PREVAI AMONG HOLSTEIN CATTLE THROUGHOUT THE WORLD, PLACING THIS DISOR AMONG THE MOST COMMON GENETIC DISBASES KNOWN IN ANIMAL AGRICULTURE. ALL CATTLE WITH THE MUTANT ALLELE ARE RELATED TO BULL, WHO THROUGH THE USE OF ARTIFICIAL INSEMINATION SIRED MAN CALVES IN THE 1950S AND 1960S.

SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.

SIMILARITY: CONTAINS 1 VWFA-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                     ; M81233; AAA30438.1; -. JC1121; JC1121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SwissProt_39:ITB2_BOVIN
                                                                                                                                                                                     IPR000561; EGF-like.
IPR002369; Integrin_B.
IPR001169; Integrin_beta_C.
IPR003659; PSI.
                                                                                                                                                       IPR002035; vWFA.
                                                                                                                      integrin_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                Integrin_B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BETA-
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S DISORDER
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alignment_block:
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SMART; SM00327; VWA; 1.
PROSITE; PS00243; INTEGRIN_BETA; 3.
PROSITE; PS00022; EGF_1; UNKNOWN_2.
PROSITE; PS01086; EGF_2; UNKNOWN_2.
Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
Repeat; Extracellular matrix; Cytoskeleton; Signal; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPAT
DISULFID
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SITE
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616 oGlyCys 618
                                                    601
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DOMAIN
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REPEAT
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                         58 GGGCTGC 64
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                                                                                                                                -684-016-48411
                                                  CysGlnCysAspProGlyTyrGlnPro...ProLeuCysSerGluCysPr 616
                                                                           TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
                                                                                                                                                                       Similarity:
                                                                                                        1/1
                                                                                                                                                                                  Quality:
Ratio:
                                                                                                        to:
                                                                                                                                                                                                                                                     ITB2_BOVIN
                                                                                                                                x ITB2_BOVIN
                                                                                                                                                                                                                                                48.50
3.731
68.421
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769
700
723
769
363
363
617
496
540
581
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                                                                                                                                                                       Percent
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BY SIMILARITY.

BY SIMILA
                                                                                                        from:
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                                                                                                                                                                                                                                                   -> G (IN LAD).
5903ADF4E8998CEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYSTEINE-RICH TANDEM REPEATS
                                                                                                       <u>بــ</u>
                                                                                                                                                                  Length: 19
Gaps: 1
Identity: 42.105
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alignment_scores:
Quality:
                                                                                                               alignment_block:
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                                                               Align seg
                                                                                             US-09-684-016-48411/rev x YCZ6_YEAST
                                                                                                                                            Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                   PROSITE; PS00463; ZN2_CY6_FUNGAL_1; 1.

PROSITE; PS00468; ZN2_CY6_FUNGAL_2; 1.

Hypothetical protein; Transcription regulation; DNA-binding; Nuclear protein; Zinc; Metal-binding.

DNA_BIND 15 42 ZN(2)-CYS(6), FUNGAL-TYPE.

SEQUENCE 832 AA; 95689 MW; 7DF91D86AF08E4E3 CRC64;
                                                                                                                                                                                                                                                                                                                                     PIR; S19418; S19418.

HSSP; P12351; 1PYC.
SGD; S0000703; YCX106W.
InterPro; IPR001138; Zn2_CY6_fungal.
Pfam; PF00172; Zn_clus; 1.
SMART; SM00066; GAL4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sonnhammer E.;
"What's in a genome?";
"What's in a genome?";
Nature 358:287-287(1992).
-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- SIMILARITY: CONTAINS 1 ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
457 IleValTrpAsnLysTyrLysPheHisValIleLeuSer...LysLeuMe
                122 GTTGTGTGGAAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTTAC 73 :::||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRESENCE OF A 2N(2)-CYS(6) FUNGAL-TYPE BINUCLEAR CLUSTER MEDLINE=92350247; PubMed=1641000; Bork P., Ouzounis C., Sander C., Scharf M., Schneider R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-MI-1999 (Rel. 38, Last annotation update)
PUTATIVE 95.7 KDA TRANSCRIPTIONAL REGULATORY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X59720; CAA42238.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grenson M., Jauniaux J.-C., Submitted (MAR-1992) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 130-832 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCZ6_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             der Linden C.G., Ma
Vliet-Reedijk J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLUSTER DOMAIN.
                                                               1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                 ţo:
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3.233
71.429
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Maurer
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                                                                 from:
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Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L.A.;
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                                                                                                                                               47.619
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CAGTCAGTGCAGC |||:::|||::: tSerAspCysThr

476

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Sed oc
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                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                        seq_name: SwissProt_39:DMSB_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name:
                                                                                                                                                                                                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                  US-09-684-016-48411/rev x YE30_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                            documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        documentation_block:
                         DMSB_HAEIN STANDARD; PRT; 205 AA. P45003; Q48049; Pel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) ANAEROBIC DIMETHYL SULFOXIDE REDUCTASE CHAIN REDUCTASE IRON-SULFUR SUBUNIT).
DMSB OR HI1046.
 Haemophilus
Bacteria; Pı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for come
ntities requires a license agreement (See http://www.isb-sib.ch/an
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YE30_CAEEL STANDARD; PRT; 156 AA 093364; P90775; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation updat HYPOTHETICAL 18.6 KDA PROTEIN C41G7.7 IN CH
                                                                                                                                                                                                                                                                                           116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS.
Jones S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z81048; CAB02843.1; -. WormPep; C41G7.7; CE08671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
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Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                      88
                                                                                                                                                                                                                                 66
                                                                                                                                                                                                                                                             72
                                                                                                                                                                                                                                                           TrpAsnAsnValHisIleSerIleThrPheGlnValLeuLeuPheThrHi 88
                                                                                                                                                                                                                                                                                        TGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTACCAGTCA 67
                                                                                                                                                                                                      sCys 89
                                                                                                                                                                                                                                 GTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SwissProt_39:YE30_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
Proteobacteria;
                                                                                                                                                                                                                                                                                                                       ţo:
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156 AA; 1
              influenzae
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                                                                                                                                                                                                                                                                                                                      YE30_CAEEL
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3.200
83.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW.
 gamma
                                                                                                                                                                                                                                                                                                                                                                                               Percent
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 subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                          Identity:
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6
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Gaps:
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IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhabditida; Rhabditoidea;
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0
50.000
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 Pasteurellaceae
                                                        (EC
                                                        1.-.-) (DMSO
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VARIANT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae dimethylsulfoxide reductase complex."
Gene 169:137-138(1996).
-!- FUNCTION: TERMINAL REDUCTASE DURING ANAEROBIC GROWTH ON VARIOUS SULFOXIDE AND N-OXIDE COMPOUNDS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Doughert B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Grine C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Wolfer C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                METAL
                                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                  PROSITE; PS0019
Oxidoreductase;
                                                                                                                                                                                                                                                                                               InterPro; IPR001450;
Pfam; PF00037; fer4;
                                                                                                                                                                                                                                                                                                                        EMBL; U32785; AAC22705.1; -.
EMBL; U26665; AAB06234.1; -.
HSSP; P00198; 1FDN.
TIGR; HI1046; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIOUS SULFOXIDE AND N-OXIDE COMPOUNDS (BY SIMILARITY).

-!- COFACTOR: IRON-SULFUR (BY SIMILARITY).

-!- SUBUNIT: THE COMPLEX CONSIST OF THREE SUBUNITS: DMSA, THI

REDUCTASE; DMSB, AN ELECTRON TRANSFER PROTEIN, AND DMSC,

MEMBRANE ANCHOR PROTEIN (BY SIMILARITY).

-!- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE

'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=EAGAN / SEROTYPE B;
MEDLINE=96186920; PubMed=8635740;
Loosmore S.M., Shortreed J.M., Co
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"Sequences of the genes encoding the A."
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MEDLINE=95350630; PubMed=7542800.
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Influenzae Rd ".
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4Fe-4S;
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              STRAIN EAGAN)
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alignment\_scores:

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seq_name: SwissProt_39:VIPR_MELGA
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               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meleagris gallopavo (Common turkey).
Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                   PROSITE: PS00649; G_PROTEIN_RECEP_F2_1; PARTIAL.

PROSITE: PS00650; G_PROTEIN_RECEP_F2_2; 1.

PROSITE: PS00650; G_PROTEIN_RECEP_F2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Vasoactive intestinal peptide stimulates prolactin mRNA expression in turkey pituitary cells: effects of dopaminergic drugs."; Proc. Soc. Exp. Biol. Med. 212:52-62(1996).
-i- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR (VIP-R) (VIP RECEPTOR)
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                                                                                                                                                                                                                                                                                                        entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS
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Ratio:
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CYTOPLASMIC (POTENTIAL).
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seq_documentation_block:
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US-09-684-016-48411/rev x VIPR_MELGA
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20-AUG-2001
TAFAZZIN.
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Q16635;
                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                  or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bione S., D'Adamo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Skeletal muscle, and Heart; MEDLINE=96224398; PubMed=8630491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A novel X-linked gene, G4.5. is responsible for Barth syndrome.";
Nat. Genet. 12:385-389(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toniolo D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                       TISSUE SPECIFICITY: HIGH LEVELS IN CARDIAC AND SKELETAL MUSCLE. UP TO 10 ISOFORMS CAN BE PRESENT IN DIFFERENT AMOUNTS IN DIFFERENT TISSUES. MOST ISOFORMS ARE BUBIQUITOUS. ISOFORMS THAT LACK THE N-TERMINUS ARE FOUND IN LEUKOCYTES AND FIBROBLASTS, BUT MOT IN HEART AND SKELETAL MUSCLE. SOME FORMS APPEAR RESTRICTED TO CARDIAC AND SKELETAL MUSCLE OR TO LEUKOCYTES.

SKELETAL MUSCLE OR TO LEUKOCYTES.

DOMAIN: THE HYDROPHILIC DOMAIN MAY SERVE AS AN EXPOSED LOOP INTERACTING WITH OTHER PROTEINS.

DISEASE: DEFECTS IN TAZ ARE THE CAUSE OF BARTH SYNDROME (BTHS), A SYNERE INHERITED DISORDER, OFTEN FATAL IN CHILDHOOD, CHARACTERIZED DISORDER, OFTEN FATAL IN CHILDHOOD, CHARACTERIZED DISORDER, OFTEN FATAL IN CHILDHOOD, CHARACTERIZED
                                                                                                                                                                                                                                                                                                                                                                                                                           THOUGHT TO BE MEMBRANE ANCHORED. SHORTEST FORMS, LACKING THE HYDROPHOBIC STRETCH, MAY BE SCLUBLE FOR TOPLASMIC PROTEINS.

ALTERNATIVE PRODUCTS: UP TO 10 ISOFORMS. SHORTER TAPAZZINS START WITH THE SECOND METHIONINE AT POS. 25. ALTERNATIVE SPLICING OF THE HYDROPHILIC CENTRAL REGION (EXONS 5-7) MAY PRODUCE 5 VARIANTS. TWO ISOFORMS, CONTAINING ALL THREE EXONS OR LACKING EXON 5 ONLY ARE CONSISTANTLY ABUNDANT. THE SEQUENCE SHOWN HERE IS THAT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysAlaMetMetValPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                LONGEST ISOFORM.
                                                                                                                                                                                             CARDIAC AND SKELETAL MYOPATHY, SHORT STATURE AND NEUTROPENIA.
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EMBL; X92763; CAA63419.1;

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seq_name: SwissProt_39:VA0D_MANSE
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                                                                                                                                                                                                                                                                                                                    025531;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel.
                                                                                                       VARSPLIC
VARSPLIC
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=97415414; PubMed=9271213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002123; Acyltransferase
InterPro; IPR000872; Tafazzin.
Pfam; PF01553; Acyltransferase; 1.
PRINTS; PR00979; TAFAZZIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
MIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative splicing;
TRANSMEM 1 3
DOMAIN 124 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
MOST OF THE ENERGY REQUIRED FOR TRANSPORT PROCESSES ACUOLAR SYSTEM.
VACUOLAR SYSTEM.
SUBUNIT: V-AATPASE IS AN HETEROMULTIMERIC ENZYME COMEDENIPHERAL CATALYTIC V1 COMPLEX (COMPONENTS A TO H)
AN INTEGRAL MEMBRANE V0 PROTON PORE COMPLEX (COMPONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgHisIleTrpAsn 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rGluLeuIleGluLysArgGlyProAlaThrProLeuIleThrValSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TrpThrLysTyrMetAsnHisLeuThrValHisAsnArgGluValLeuTy
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snHisGlnSerCysMetAspAspProHisLeuTrpGlyIleLeuLysLeu
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300069; -
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Ratio:
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CAA63418.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFZ_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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1.920
45.455
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194
153
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                                            HETEROMULTIMERIC ENZYME COMPOSED OF
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MISSING (IN
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Gaps:
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  (COMPONENTS: A, C,
                        TO H) ATTACHED
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                 "Absence of mutations involving the gene LHX9 in 46,XY agenesis and dysgenesis.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: INVOLVED IN GONADAL DEVELOPMENT (BY SIMILA-
-i- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-i- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9NQ59; Q9NQ70;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LIM/HOMEOBOX PROTEIN LHX9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X98825; CAA67343.1; -.
InterPro; IRR002843; VATP-Synt_AC39.
Pfam; PF01992; VATP-Synt_AC39; 1.
Hydrolase; Hydrogen ion transport.
SEQUENCE 348 AA; 39596 MW; 016BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 laAlaThrProAlaGluLeuTyrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 LeuLeuIleThrGlyThrLeuHisGlnArgProIleSerGluLeuIlePr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C'' AND D).
-!- SIMILARITY: BELONGS TO THE V-ATPASE VOD/AC39 SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 GTTGTAAGGCATCTCACATTTACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 TCGCATTGCGCCATTAGGT.....
                                                                                                                                     SIMILARITY: CONTAINS 2 LIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SwissProt_39:LHX9_HUMAN
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2.182
52.381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                     DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149
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                                                                                                                                     THE
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                                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
                                                                                                                                     LIM
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1
30.952
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                                                                                                                                                                                                                                                                    46, XY gonadal
                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
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non-profit institution and this statement is

not removed.

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alignment_block:
US-09-684-016-48411/rev x LHX9_HUMAN
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                                                                                                                                                                                                                                                                                                                                    seq_name: SwissProt_39:LHX9_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00046; homeobox; 2.
Pfam; PF000412; LIM; 3.
ProDom; PD000094; LIM; 2.
SMART; SM00389; HOX; 1.
SMART; SM00382; LIM; 2.
PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS50027; HOMEOBOX_1; 1.
PROSITE; PS00027; HOMEOBOX_2; 1.
PROSITE; PS00027; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AJ277916; CAB98128.1; ALT_SEO.
EMBL; AJ277917; CAB98128.1; JOINED.
EMBL; AJ277918; CAB98128.1; JOINED.
EMBL; AJ277919; CAB98128.1; JOINED.
EMBL; AJ277919; CAB98128.1; JOINED.
EMBL; AJ277920; CAB98128.1; JOINED.
InterPro; IPRO01356; Homeobox.
InterPro; IPRO01781; LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metal-binding; Z.
DOMAIN 62
DOMAIN 124
DNA_BIND 258
SEQUENCE 388 A
                                                                                                                                                                                                                                                                                                           documentation_block:
                                                                                                                                                                                                                              LHX9_MOUSE STANDARD; PRT; 388 AA.
09WUH2; O9WU44; Q90YQ5; Q9QX00;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LIM/HOMEOBOX PROTEIN LHX9.
                                                                          MEDLINE=99098964; PubMed=9880598;
Retaux S., Rogard M., Bach I., Failli V.,
"Lhx9: a novel LIM-homeodomain gene expres
forebrain.";
                                                                                                                              SEQUENCE OF 1-300 FROM N.A. STRAIN=C57BL/6;
                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
             STRAIN=NIH SWISS;
MEDLINE=99264291; PubMed=10330499;
                                                                                                                                                                                                                                                                                                                                                              161
                                                                                                                                                                                                                                                                                                                                                                                                                145
                                      SEQUENCE OF 11-388 FROM N.A.
                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                        96
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                                                                  Neurosci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
Similarity:
                                                                                                                                                                                                                                                                                                                                                                               CATTAGGTCATCAGGGTTGTAAGGCATCTCACATTTAC 9
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                                                                                                                                                                                                                                                                                                                                                                                                              TyrHisLeuSerCysPheThr.CysSerThrCysAsnLysThrLeuThrT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                       TATCACCTTACATGTGAAACTTACCAGTCAGTGCAGCCCTCGCATTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJ277915;
 S., Porter F.D., Pitts A.,
                                                               19:783-793(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHX9_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zinc.
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2.824
56.667
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177
317
42903
                                                                                                                                                                               Chordata;
Rodentia;
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A4DC8B914D7C3B66
                                                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
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Gaps:
Identity:
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6
Kumar M.,
                                                                                      li V., Besson expressed in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
1
40.000
                                                                                                                                                                               Muridae;
Agulnick A., Wassif C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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                                                                                      M.J.;
the developing
                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain;
                                                                                                                                                                              Murinae; Mus
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alignment_scores:
    Quality:
                                                                                                                        STATES AND ARREST AND COLOR OF THE PROPERTY OF
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EMBL; AF113518; AAD22008.1; -.
EMBL; A7243851; CAB59907.1; -.
EMBL; A7243852; CAB59908.1; JOINI
EMBL; A7243853; CAB59908.1; JOINI
EMBL; A7243855; CAB59908.1; JOINI
EMBL; A7243855; CAB59908.1; JOINI
EMBL; A7243855; CAB59908.1; JOINI
EMBL; A7243855; CAB59909.1; JOINI
EMBL; A7243855; CAB59909.1; JOINI
EMBL; A7243855; CAB59909.1; JOINI
EMBL; A7243855; CAB59909.1; JOINI
EMBL; A7243857; CAB5909.1; JOINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00412; LIM; 2.
ProDom; PD000094; LIM; 2.
SMART; SM00389; HOX; 1.
SMART; SM00382; LIM; 2.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50073; LIM_DOMAIN_1; 2.
PROSITE; PS500478; LIM_DOMAIN_2; 2.
PROSITE; PS50043; LIM_DOMAIN_2; 2.
                                                                                                                 CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                       Homeobox; DNA-binding; Nuclear protein; Remetal-binding; Zinc; Alternative splicing.

DOMAIN 62 114 LIM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1316721; Lhx9.
InterPro; IPR001356; Homeobox.
InterPro; IPR001781; LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb·sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
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                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00046; homeobox; 1. Pfam; PF00412; LIM; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=20221375; PubMed=1075
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                                                                                                                     A -> T (IN REF. 2).
S -> F (IN REF. 2).
; C2D7326A68D87B32 CRC64;
                                                                                                                                                                                                                          HOMEOBOX.

VWEQNARAKERRNLLRQENGGVDKADGTSLPAPPSADSGAL

TPPGTATTLTDLTNPTVTTVVTTVISNNDSHEEGSPSGTTLT

NLE -> GEQILGHYSQTSRRLKIP (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                               LIM 2
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cerebral cortex.";
                                                                                                                                                                                                           ALPHA).
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Ratio: Percent Similarity:

48.00 2.824 56.667

Length: Gaps: Percent Identity:

30 1 40.000

alignment\_block:

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seq_name:
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                                                                                            InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; death; 1.
Pfam; PF00201; TNFR_c6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR_NGFR_1; 3.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS00050; TNFR_NGFR_2; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P18519;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation updat
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR F
(GP80-LNGFR) (P75 ICD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
NGFR_CHICK STANDARD;
 DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                       PIR; JN0006; JN0006.
PIR; A60504; A60504.
HSSP; P07174; INGR.
                                                 CHAIN
                                                           Phosphorylation;
SIGNAL 1
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-I- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO
                                                                                                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 21-416 FROM N.A. MEDLINE=90152140; PubMed=2154393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Large T.H., Weskamp
Shooter E.M., Reicha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                    Neuron 2:1123-1134(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure and developmental expression receptor in the chicken central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90166579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archosauria;
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                                                                                                                                                                                                                                           PTM: N- AND O-GLYCOSYLATED AND IS PH
SIMILARITY: CONTAINS A LA-NGFR/TNFR-
SIMILARITY: CONTAINS 1 DEATH DOMAIN
                                                                                                                                                                                                                                                                                            NT-3, AND NT-4.
SUBUNIT: NGF RECEPTOR
BOND FORMATION.
                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATTAGGTCATCAGGGTTGTAAGGCATCTCACATTTAC
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                                                                                     Neurogenesis;
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Reichardt L.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A.
                                                                     Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *v, Last annotation update)
E GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
ICD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=2560385;
 239
261
416
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                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helder J.C.,
                                                                                                                                                                                                                                                                                                         CAN FORM
                                                                                                                                                                                                                                                         ATED AND IS PHOSPHORYLATED ON SERINE.
LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
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                                   POTENTIAL.
LOW-AFFINITY
RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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0:
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                                                                                   Glycoprotein;
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                                                NERVE
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                                                                                                                                                                                                                                                                                                                                                                    Bothwell M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 nerve growth
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                                                                                                                                                                                                                                                                                                        THROUGH
                                                                                                                                                                                                                                                                                                                                                        chicken
                                                GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misko T.P
                                                                                   Repeat;
                                                                                                                                                                                                                                                                                                                                NGF,
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                                                                                                                                                                                                                                                                                                         DISULFIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phasianinae;
                                                                                                                                                                                                                                                                                                                               BDNF,
                                                                                                                                                                                                                                                                                                                                                       receptor.";
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Sequence of the control of the contr
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US-09-684-016-48411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: SwissProt_39:NGFR_RAT
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SEQUENCE
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01-APR-1988 (Rel. 07, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR
(GP80-LNGFR) (P75 ICD):
                                                       TISSUE-Liver;
MEDLINE-93077038; PubMed=1446821;
                                                                                                                                                                                                                                                  MEDLINE-87115859; PubMed=3027580;
MadDLINE-87115859; PubMed=3027580;
Radeke M.J., Misko T.P., Hsu C., Herz
"Gene transfer and molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115
                                Metsis
                                                                                                                                                                                                                            receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
                                                                                                                              SEQUENCE OF 1-22
                                                                                                                                                                                              Nature
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
'Regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
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                                                                                                                                                                                                                               transfer
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                                   Timmusk
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   fimmusk T., A. elements and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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65.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
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   llikmets R., Saarma transcriptional re
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BY SIMILARITY.

BY SIM
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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loning of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6BCEAAB54F4D2D56
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FR-CYS 1.
FR-CYS 2.
FR-CYS 3.
FR-CYS 4.
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Gaps:
Identity:
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                                                                                                                                                                                                                                                                                      Shooter
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Murinae; Rattus.
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         testosterone
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alignment_scores:
                                                                                            DOMAIN
DISULFID
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DOMAIN
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97449145; PubMed=9305641; Liepinsh E., Ilag L.L., Otting G., Ibanez C.F.; "NMR structure of the death domain of the p75 neuro EMBO J. 16:4999-5005(1997).

-!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND NT-3, AND NT-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00005; DEATH; 1
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 334-418
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SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOND FORMATION.
SUBCELLULAR LOCATION: TYPE
PTM: N- AND O-GLYCOSYLATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00531; death; 1. PF00020; TNFR_c6; 4.
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   Quality:
Ratio:
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DEATH.

BY SIMILARITY.

BY SIMILARITY.
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CYSTEINE-RICH REGION
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 alignment_block:
US-09-684-016-48411
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EMBL;
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"Gene structure and
(GABRG3) gene.";
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                 S82769; AAB39369
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seq_name: SwissProt_39:GAC3_HUMAN
use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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15-JUL-1998 (Rel. 36, Created)
20-AUG-2001 (Rel. 40, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA
                                                                                                                                                                                                                                                                                 Submitted (JAN-2000) to the EMBL/
-i- FUNCTION: GABA, THE MAJOR IN-
VERTEBRATE BRAIN, MEDIATES NE
GABA/BENZODIAZEPINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal brain;
MEDLINE=96360042; PubMed=8719414;
                                                                                                                                                                                                                                                                                                                                                           "Genomic organization (GABRG3).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression and pharmacology of human GABAA receptors containing
                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                       SUBUNIT: GENERALLY PENTAMERIC. THERE ARE RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DEL SUBCELLULAR LOCATION: INTEGRAL MEMBRANE MISCELLANEOUS: THIS SUBUNIT CARRIES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CysArgCysAlaTyrGlyTyrTyrGlnAspGluGluThrGlyHisCysGl
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etazoa; Chordata;
theria; Primates;
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MAJOR INHIBITORY NEUROTRANSMITTER IN THE INDIATES NEURONAL INHIBITION BY BINDING TO TAKE THE APPLIATES NEURONAL INHIBITION BY BINDING TO TAKE THE APPLIANCE AN INTEGRAL CHLORIDE
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                                                                                                                                                                                                                                                                                                                                                                                                               Z.-Y.,
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                                                               as its content
                        http://www.isb-sib
                                                                                                                                                                                                            RE FIVE TYPES ELTA, AND RHO. PROTEIN.
                                                                                                                                                                                           BENZODIAZEPINE
                                          Usage
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Homo.
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alignment_block:
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                                                                                                                                                                                                                                              Percent Similarity:
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CARBOHYD
CARBOHYD
DISULFID
CONFLICT
SEQUENCE
                                                                                      documentation_block:
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TRANSMEM
TRANSMEM
                      MM17_HUMAN STANDARD; PRT; 606 AA.
Q9UL29; Q14850;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
MATRIX METALLOPROTEINASE-17 PRECURSOR (EC 3.4.24.-)
(MEMBRANE-TYPE MATRIX METALLOPROTEINASE 4) (MT-MMP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
EMBL;
EMBL;
        MATRIX METALLOPROTEINASE)
MMP17 OR MT4MMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
Homo
                                                                                                                            169
                                                                                                                                                               153
                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00252; NRIONCHANNEL. PRINTS; PR00253; GABAARECEPTR.
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00065;
                                                                                                                                                                                                                                                                                                                                                         NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                             69
                                                                                                                                                                                                  seg 1/1
                                                                                                                                                             IleTrpAsnAspGlyLysIleLeuTyrThrLeuArgLeuThrIleAsnAl
                                                                                                                                                                               GTGTGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTACCAG
                                                                                                                          aGluCysGlnLeuGlnLeuHisAsnPheProMetAspGluHisSerCys
                                                                                                                                            TCAGTGCAGCCCTCGCATT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            600233;
sapiens
                                                                                                         SwissProt_39:MM17_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF228453;
AF228454;
AF228455;
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AF269136;
AF269138;
AF269138;
AF269140;
AF269141;
AF269141;
AF228458;
AF228458;
AF228458;
AF228451;
                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                o; IPR001175; Neur_chan
f00065; neur_chan; 1.
PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                              family; Transmembrane.
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6
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467
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255
281
315
315
338
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444
110
228
                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                GAC3_HUMAN
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                 (MT4-MMP)
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T -> P (IN REF. 1).
: 1B22D145166438D6 CRC64;
                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                       PROBABLE.
CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                           GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
                                                                                                                                                                                                                                                                                                                                                                          PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                  PROBABLE
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Identity:
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6
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1
27.273
                       ) (MMP-17)
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                         (MEMBRANE-TYPE-4
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type 4 ma
J. Biol.
the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                           This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Membrane type 4 matrix metalloproteinase (MT4-MMP, glycosylphosphatidyllnositol-anchored proteinase."; J. Biol. Chem. 274:34260-34266(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 matrix metalloproteinase.";
Biol. Chem. 380:1103-1108(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20008793; PubMed=10543448; Kolkenbrock H., Essers L., Ulbrich N., "Biochemical characterization of the c 4 matrix metalloproteinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 129-302 FROM N.A., AND CHARACTERIZATION MEDLINE=20020281; PubMed=10551873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Monocytic leukemia; MEDLINE=99402951; PubMed=10471807;
                                                                                                                                                                                                                                                                                                   -!- PTM: THE PRECURSOR IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20036570; PubMed=10567400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang Y., Johnson A.R., Ye Q.-Z., Dyer R.D.; "Catalytic activities and substrate specificity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer Res. 56:944-949(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Puente X.S., Pendas A.M., Llano E., Velasco "Molecular cloning of a novel membrane-type from a human breast carcinoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Breast carcinoma; MEDLINE=96234364; PubMed=8640782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for human and mouse mt4-mmp transcripts."; FEBS Lett. 457:353-356(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by a novel major transcript: isolation of complementary DNA
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                                                                                                                                                                                                                                                                                                                     PROTEOLYTICALLY ACTIVATES PROGELATINASE A. DOES NOT HYDROLYSE COLLAGEN TYPES I, II, III, IV AND V, GELATIN, FIBRONECTIN, LAMININ, DECORIN NOR ALPHA1-ANTITRYPSIN.

CATALYTIC ACTIVITY: CLEAVES PRO-TNF-ALPHA AT THE 74-ALA-|-GLN-75 SITE.

COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY (BY SIMILARITY).

SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT/PUENTE-TYPE FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EXPRESSED IN BRAIN, LEUKOCYTES, COLON, OVARY TESTIS AND BREAST CANCER. EXPRESSED ALSO IN MANY TRANSFORMED AND NON-TRANSFORMED CELL TYPES.
                                                                                                                                                                           SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
                                                                                                                                                                                                               SIMILARITY).

SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: ENDOPEPTIDASE THAT DEGRADES VARIOUS COMPONENTS OF THE EXTRACELLULAR MATRIX, SUCH AS FIBRIN. MAY BE INVOLVED IN THE ACTIVATION OF MEMBRANE-BOUND PRECURSORS OF GROWTH FACTORS OR INFLAMMATORY MEDIATORS, SUCH AS TUMOR NECROSIS FACTOR-ALPHA. MAY ALSO BE INVOLVED IN TUMORAL PROCESS. NOT OBVIOUS IF ABLE TO
                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 matrix metalloproteinase catalytic domain. iol. Chem. 274:33043-33049(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ., Will H.; catalytic domain
                                 There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Itoh
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                                                                                             EMBL outstation
                                                                                                                        a collaboration
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

n no way

MIM; 602285;

Hemopexin.

AB021225; BAA82707.1; X89576; CAA61753.1; -P08254; IUSN. M10.017; -.

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seq_documentation_block:
ID APC2_CAVPO STANDA
AC P27916;
DT 01-AUG-1992 (Rel. 23,
DT 01-AUG-1992 (Rel. 23,
DT 01-NUG-1995 (Rel. 23,
DT 01-NUG-1995 (Rel. 32,
DT 01-NUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: MM17_HUMAN
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                                  P27916;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updata
APOLIPOPROTEIN C-II PRECURSOR (APO-CII)
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CONFLICT
SEQUENCE
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ACT_SITE
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CHAIN
PROPEP
DOMAIN
  Cavia porcellus (Guinea pig).
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Pfam; PF00045; hemopexin; 4.
Pfam; PF00413; Peptidase_M10; 1.
PRINTS; PR00138; MATRIXIN.
                                                                                                                                                                                                                                                                                                                      146
                                                                                                                                                                                                                                                                                                                                                                                                                                       116 TGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTACCAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Metalloprotease; Zinc; Calcium; Zymogen; Sig GPI-anchor; Extracellular matrix; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
PROSITE; PS00024; HEMOPEXIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00120; HX; 4.
SMART; SM00235; ZnMc; 1.
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InterPro; IPR001818;
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2.526
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N-LINKED (GLCNAC. . .) (POTENT
MISSING (IN SHORT ISOFORM).
GPGGTV -> ARRHR (IN REF. 1).
D -> Y (IN REF. 1).
D -> N (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC (CATALYT)
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPI-ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYSTEINE SWITCH (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MATRIX METALLOPROTEINASE-17 REMOVED IN MATURE FORM (POT
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BY SIMILARITY
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                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> Y (IN REF. 1).
-> N (IN REF. 1).
F3BF2EF21918F44C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to:
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                                                                                                                                         100
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                                                           update)
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seq_name: SwissProt_39:EGIP_ANTCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
TISSUE-Embryo;
TISSUE-Embryo;
MEDLINE-95220383; PubMed-7705369;
Yamasu K., Watanabe H., Kohchi C., Soma G.-I., Mizuno D.-I.,
Yamasu K., Shimada H., Suyemitsu T., Ishihara K.;
Akasaka K., Shimada H., Suyemitsu T., Ishihara K.;
"Molecular cloning of a CDNA that encodes the precursor to several
"Molecular cloning of a CDNA that encodes the precursor to several
                                                                                                                                                                                                                                                            EGIP_ANTCR STANDARD; PRT; 325 AA.

P15217; P15218; P15219;

01-APR-1990 (Rel. 14, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

01-OCT-1996 (Rel. 34, Last annotation update)

EXOGASTRULA-INDUCING POLYPEPTIDE PRECURSOR (EGIP).
                                                                                                                                                                                                                                                                                                                                                                                 documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
SEQUENCE
                                                                                                                                                                      Anthocidaris.
NCBI_TaxID=7629;
                                                                                                                                                                                                                              Anthocidaris crassispina (Sea urchin). Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Characteristics, cDNA sequence, and tissue expression.";

J. Biol. Chem. 266:4074-4080(1991).

-i. FUNCTION: APOC.-II IS A COMPONENT OF THE VERY LOW DENSITY

-i. FUNCTION: APOC.-II IS A COMPONENT OF THE VERY LOW ACTIVATOR OF

ELPOPROTEIN (VLDL) FRACTION IN PLASMA, AND IS AN ACTIVATOR OF

SEVERAL TRIACYLGIZCEROL LIPASES. THE ASSOCIATION OF APOC.-II WITH

PLASMA CHYLOMICRONS, VLDL, AND HDL IS REVERSIBLE, A FUNCTION OF

THE SECRETION AND CATABOLISM OF TRIGLYCERIDE-RICH LIPOPROTEINS,
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                             Echinoidea; Euechinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chylomicron; VLDL; Plasma; Lipid transport; Lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A38685; A38685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M59913; AAA37031.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andersson Y., Thelander L., Bengtsson-Olivecrona G.; "Demonstration of apolipoprotein CII in guinea pigs. Functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-91154195; PubMed=1999402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAGTTTCACATGTAAGGTGATACTTATCTT 104
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Identity:
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                                                                                                                                                                                                                 Echinometridae;
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alignment_scores:
Quality:
Ratio:
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Repeat;
SIGNAL
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PROSITE: PS00022; EGF_1; FALSE_NEG.

PROSITE: PS00022; EGF_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a celebrate the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The exogastrula-inducing peptides in embr
Anthocidaris crassispina -- isolation and
structure.";
                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 2.
SMART; SM00001; EGF; 2.
SMART; SM00001; EGF_like; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Amino acid sequence of exogastrula-inducing peptide C from the urchin, Anthocidaris crassispina.";
Biochim, Biophys, Acta 999:24-28 (1989),
-i- FUNCTION: THE EGIP PEPTIDES ARE FACTORS EFFECTIVE TO EXTRUDE ARCHENTERON TOWARD OUTSIDE OF EMBRYOS. MAY HAVE A ROLE IN THE TUDICATION OF TAXTERIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89230051; PubMed-2713739; Suyemitsu T., Asami-Yoshizumi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90028385; PubMed-2804137;
Suyemitsu T., Tonegawa Y., Ishihara K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 47-104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 106-158 AND 179-230.
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Eur. J. Bioch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishihara K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDUCTION OF GASTRULATION.
SIMILARITY: EACH OF THE 4 PEPTIDES CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                              ; Z48184; CAA88234.1;
A48167; A48167.
B48167; B48167.
S06637; S06637.
                                                                                                                                                                                                                                                                                                                                                                                                                     P00592;
                                                                                                                                                                                                                                                                                                                        Gastrulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tides of the sea urchin Anthocidaris crassispina."; Biochem. 228:515-523(1995).
                                                                                 140
184
191
213
256
263
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106
179
251
48
107
1180
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                                                             Ą,
47.50
3.393
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154
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                                                                   EXOCASTRULA-INDUCING P

EXOCASTRULA-INDUCING P

EXOCASTRULA-INDUCING P

EXOCASTRULA-INDUCING P

EGIP-X (PROBABLE).

EGF-LIKE 1.

EGF-LIKE 3.

EGF-LIKE 3.

EGF-LIKE 4.

BY SIMILARITY.

BY SIMILARITY.
                                                           1FD2577B3617306A CRC64;
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 Length:
Gaps:
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and determination o
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                                                                                                                                                                                                                                                                                                                                   Extracellular
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PEPTIDE
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of the pi
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(EGIP-D)
(EGIP-A)
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alignment_block:
US-09-684-016-48411 x EGIP_ANTCR
                                                                                                                            Align seg
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107 hrValAlaArgCysGlu 112
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                    TAATGGCGCAATGCGAG
                                                                                                      TATTGTAAATGTGAGATGCCTTAC...............
                                       sTyrMetProLysAspLysGluGluAspValGluIleGluThrLysAspT 107
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                                                                                                                            EGIP_ANTCR
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                     58
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Q24459 drosophila melanog ! Q9v8c2 drosophila melano

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sp_human:Q9HAH2
sp_human:Q9UPP1
sp_fung1:Q03012
sp_fung1:Q74508
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sp_invertebrate:09NLC1 + 62.00 154.6

sp_invertebrate:045407 + 62.00 153.8

sp_invertebrate:045407 + 60.00 136.79

sp_human:014687 + 60.00 132.90

sp_human:014686 + 60.00 132.49

sp_human:014686 - 60.00 132.49
                                                                                                                                                              sp_human:Q9NR48 +
sp_human:Q9H0S7 +
sp_invertebrate:Q9XWD7
sp_plant:Q9FNI5 +
                                                                                                                                                                                                                                                                                                                                                                                                                            sp_rodent:Q9WV00
sp_vertebrate:Q9W664
sp_human:015043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search information block:
Query: US-09-684-016-48411
Query length: 123
Database: SPTREMBL_17:*
                                                                                   sp_invertebrate:09U263
sp_invertebrate:044498
                                                                                                                                                                                                                                                                                                                                                         sp_human:Q9H4G6
sp_archea:Q9YEG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_human:Q9BQW0
sp_human:Q9BW03
sp_human:Q9NUM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_plant:Q9T0A1 +
sp_invertebrate:Q9VRV6
sp_fungi:Q9UT79 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database sequences: 473505
Database length: 146272329
Search time (sec): 65.740000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_human:Q9BTC0
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sp_plant:Q9XJ51
sp_rodent:Q9WTU0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_invertebrate:Q22662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_human:Q9Y6N4 + sp_invertebrate:Q9VJE3
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sp_plant:Q9FEN9
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=pfs
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09684016_@CGN1_1_96 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -MODEL=frame+_n2p.model -DEV=xlh
-Q=/Cgn2_1/USPTO_spool/USO9684016/runat_19032002_084440_20931/app_query.fasta_1.182
-DB=SPTREMBL_17 -QFMT=fastan -SUFFIX=std.rspt -GAPOP=12.000
-GAPEXT=4.000 -MINANTCH=0.100 -LOOPCL=0.000 -LOOPEXT=-0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
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66.50 169.00 0.1089
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1 Documentation

1 1 05462 arabidopsis thaliana (mc)

27 1 043479 hordeum vulgare (barley)

28 1 09fen9 arabidopsis thaliana (mc)

8 1 09svi4 arabidopsis thaliana (mc)
                                       | Q9fni5 arabidopsis thaliana (m
| 15 | Q9u263 caenorhabditis elegan
| 15 | Q9u263 caenorhabditis elegan
| 15 | Q4u498 caenorhabditis elegan
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                                       sp_plant:Q43479
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sp_invertebrate:Q9VG78 +
sp_virus:Q98VX5 +
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065462 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL102140; CAA18117.1; -.
EMBL; AL16156; CAB79169.1; -.
Mendel; 29749; Arath; 2000; 29749.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RECEPTOR LIKE PROTEIN (FRAGMENT).
F1N20.240 OR AT4G22140.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01426; BAH; 1.
Pfam; PF00628; PHD; 1.
SMART; SM00439; BAH; 1.
SMART; SM00249; PHD; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
SEQUENCE 201 AA; 22979 MW; 4C48
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
The H., Wambutt R.,
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                                                                           115 TyrCysLysCysGluMetProTyrAsnProAspAspLeuMetValGlnCy
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InterPro; IPR000561; EGF-like
InterPro; IPR001965; PHD.
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Mayer K.F.X.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                  5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
sGluGlyCysLysAspTrp
                                        CGAGGGCTGCACTGACTGG
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Grymonprez B., Volckaert G, Mewes H.W., Lemcke
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Q9fk65 arabidopsis thaliana
! Q9vg78 drosophila melano
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alignment_scores:
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US-09-684-016-48411 x Q43479
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Q43479 PRELIMINARY;
Q43479;
Q1-01-NOV-1996 (TrEMBLrel. 0:
01-NOV-1996 (TrEMBLrel. 0:
01-JUN-2001 (TrEMBLrel. 1:
                                                                                                                                                                                                                                         _documentation_block:
Q9FEN9 PRELIMINARY;
Oh M., Torisky k.s., ....

"PHD Finger Dependent Binding of SHL1 to a spearabidopsis TCH4 in vitro.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
EMBL; AF277453; AAG21353.1;

InterPro; IPR001025; BAH.

InterPro; IPR001025; BAH.
                                                                                                                                                                                          Q9FEN9;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Plant Sci. 106:91-98(1995).
EMBL; X77575; CAA54682.1; -
                                                                                                                                                                                PUTATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01186; EGF_2; UNKNOWN_1.
SMART; SM00439; BAH; 1.
SMART; SM00249; PHD; 1.
SMART; SM00249; PHD; 1.
SEQUENCE 227 AA; 25741 MW; ECLA
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InterPro; IPR000561; EGF-like.
InterPro; IPR001025; BaH.
InterPro; IPR001965; PHD.
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Triticeae; Hordeum.
                                                                                   SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=3702;
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Eukaryota; Viridiplantae;
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(TrEMBLrel. 17, Last annotati
D FINGER TRANSCRIPTION FACTOR.
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US-09-684-016-48411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
    Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 01-MAY-2000 (TrEMBLrel. 13, Created)
T 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
T 01-UN-2001 (TrEMBLrel. 17, Last annotation update)
E ES43 LIKE PROTEIN (FRAGMENT).

N F19H22.200 OR AT4G39100.
S Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trace curosids II; Brassicales; Brassicaceae; Arabidopsis.
(NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
BEVAN M., Murphy G., Ridle
Bevan M., Schueller C
Mayer K.F.X., Schueller C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001965; PHD.
Pfam; PF01426; BAH; 1.
Pfam; PF00628; PHD; 1.
SMART; SM00439; BAH; 1.
SMART; SM00249; PHD; 1.
SMART; SM00249; PHD; 1.
PROSITE; PS00322; HISTONE_H3_1; UJ
SEQUENCE 228 AA; 26122 MW; A89
                                              InterPro; IPR000
InterPro; IPR000
Pfam; PF01426;
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Q9SVI4 PRELIMINARY;
    Pfam; 1
Pfam; 1
SMART;
                                                                                                                                                              EU Arabidopsis sequencing proj
Submitted (MAR-2000) to the EM
EMBL; AL035679; CAB38830 1; -.
EMBL; AL161594; CAB80573.1; -.
                                                                                                                                                                                                                                                                                                                                 Zimmermann
Smith A., 1
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Murphy G., Ridley P.,
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing pusubmitted (MAR-1999) to the
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01-MAY-2000
                                                                                                                                                                                                                                                                                                             Submitted
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                                                                                                                  InterPro;
                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; IPR001025; BAH.; IPR0010551; EGF-11ke.; IPR000154; Histone_H3.; IPR000155; PHD.
01436; BAH; 1.
006238; PHD; 1.
                                                                                                                                                                                                                                                                                                        n W., Grueneisen A., Wambutt R., Kalicki J.,
Mewes H.W., Lemcke K., Mayer K.F.X.;
(MAR-2000) to the EMBL/GenBank/DDBJ database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to:
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Gaps:
Percent Identity:
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ne EMBL/GenBank/DDBJ
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EMBL/GenBank/DDBJ
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J databases
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\_2; UNKNOWN\_1.

UNKNOWN\_1.

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alignment_block:
US-09-684-016-48411 x Q9XJ51
                                                                                                                                                                 alignment_scores:
Quality:
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DR
FT
SQ
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                                                                                                                                            Ratio:
Percent Similarity:
                                                                                      Align seg 1/1
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                                                                                                                                                                                                                                        STRAINCHINES SPRING; TISSUE-ROOT;
STRAINCHINESE SPRING; TISSUE-ROOT;
Nemoto Y., Kawakami N., Sasakuma T.;
"Isolation of novel early salt-responding genestivum L.) by differential display.";
Theor. Appl. Genet. 98:673-678(1999).
EMBL; AB011445; BAA82157.1;
InterPro; IPR001965; PHD.;
Pfam; PF00628; PHD; 1.
SMART; SM00249; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           documentation_block:
Q9XJ51 PRELIMINARY;
                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00249; PHD; 1.
PROSITE; PS01186; EGF_2; UNKNOWI
PROSITE; PS00322; HISTONE_H3_1;
NON_TER 258 258
SEQUENCE 258 AA; 29675 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                 Triticum aestivum (Wheat).
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                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4565;
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                     73
17 p 17
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                     G 73
                                         Similarity:
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AA;
                                                                                       Q9xJ51 from:
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5.636
95.652
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6.125
94.118
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                                                                                                                                           Identity:
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Gaps:
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88.235
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78.261
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SOON BEACH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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09WTU0 PRELIMINARY;
09WTU0; PRELIMINARY;
01-NOV-1999 (TrEMBLrel. 12, C
01-NOV-1999 (TrEMBLrel. 12, L
01-JUN-2001 (TrEMBLrel. 17, L
SEQUENCE FROM N.A.

MEDLINE-99160472; PubMed-10051327;

Hasenpusch-Theil K., Chadwick B.P., Theil

Wilkinson D.G., Frischauf A.M.;

"PHF2, a novel PHD finger gene located or

Mamm. Genome 10:294-298(1999).

EMBL; AF043725; AAD21791.1;

InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                             documentation_block:
                                                                                                                    Homo sapiens (Human).
Homo sapiens (Human).
'``rvota; Metazoa; Chordata; '
                                                                                                                                                                                           Q9Y6N4 PRELIMINARY;
Q9Y6N4;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO00561; EGF-1ike.
InterPro; IPRO01965; PHD.
Pfam; PF00628; PHD; 1.
SMART; SM00249; PHD; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
SEQUENCE 1096 AA; 120798 MW; D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99160472; PubMed=10051327;
Hasenpusch-Theil K., Chadwick B.P., Theil
Wilkinson D.G., Frischauf A.M.;
"PHF2, a novel PHD finger gene located on
Mamm. Genome 10:294-298(1999).
EMBL; AF043726; ABD21792.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                   PHD-FINGER PROTEIN.
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                                                                                                                                                                                                                                                                                                               sAspAlaCysLysAspTrp
                                                                                                                                                                                                                                                                                                                                      CGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                 TyrCysValCysArgLeuProTyrAspValThrArgPheMetIleGluCy
                                                                                                                                                                                                                                                                                                                                                                                          TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
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Ratio:
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4.529
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Gaps: 0
Percent Identity: 43.478
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Last sequ
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Last annotation updat
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Last annotation update)
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                                                                                                                               Craniata; Vertebrata; Catarrhini; Hominidae;
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RX MEDLINE-20196006; PubMed-10731132;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Adbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Benos P.V., Berman B.P., Bhandari D., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
             TRAPA
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DR
SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-016-48411 x Q9Y6N4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VJE3; PRELIMINARY;
Q9VJE3;
Q1-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
CG15141 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00628; PHD; 1
PROSITE; PS01186; EGF
SMART; SM00249; PHD;
SEQUENCE 1099 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001965; PHD
Pfam; PF00628; PHD; 1.
PROSITE; PS01186; EGF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrCysValCysArgLeuProTyrAspValThrArgPheMetIleGluCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophilidae; Drosophila.
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4.529
73.913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 1.
121063 MW; DA1AD9826FFF3B77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
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13,
17,
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Gaps: 0
Percent Identity: 43.478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Weinley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Wyers E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RI Science 287:2185-2195(2000).
EMBL; AE003655; AAF33607.1; -.
DR FANAL; AE0031265; PHD.
DR InterPro; IPR0013265; PHD.
DR InterPro; IPR001326; PHD; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00249; PHD; 1.
SQ SEQUENCE 404 AA; 45969 MW; 467FB27F9F97E995 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-016-48411 x Q9VJE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _documentation_block:
Q9HAH2 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TremBLrel. 16, Created)
01-MAR-2001 (TremBLrel. 16, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
CDNA FLJ11634 FIS, CLONE HEMBA1004275, MODERATELY SIMILAR TO HOMO
SAPIENS PHD-FINGER PROTEIN (GRC5) MRNA (FRAGMENT).
                                                                                                                                                                                              Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara I Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yanamoto J., Wakamata Y., Nagahari K., Yanamoto J., Wakamata Y., Nagahari K., Yanamoto J., Yanamata Y., Nagahari K., Yanamata Y., Nagahari K., Yanamata Y., Nagahari K., Yanamoto J., Wakamata Y., Nagahari K., Yanamata Y., Nagahari K., Yanamata Y., Nagahari K., Yanamata Y., Nagahari K., Yanamata Y., Nagaha
                             PROSITE; PS01186; EGF_2; UNKNOWN_1.
NON_TER 790 790
                                                                                      Pfam; PF00628; PHD; 1
SMART; SM00249; PHD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-WHOLE EMBRYO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 TyrCysLysCysLysArgProTyrProAspProAspArgThrValGluGl 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 uValMetLeuGlnCysAlaIleCysGluAspTrp
                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 CCTAATGGCGCAATGCGAGGGCTGCACTGACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                           IPR000561; EGF-like.
IPR001965; PHD.
  790 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9VJE3 from: 1
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4.250
64.286
  88642 MW; D4D21D2A766C671A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAINLY HEAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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2
50.000
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seq_documentation_block:
                       seq_name:
                                                                                                                                                               alignment_block:
US-09-684-016-48411 x Q9UPP1
                                                                                                                                                                                                                         alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: sp_human:Q9UPP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-684-016-48411 x Q9HAH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                          Align
                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              documentation_block:
Q9UPP1 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           Kikuno R., Nagase T., Ishikawa K., Hirosawa M., Miya
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified
The complete sequences of 100 new cDNA clones from k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                           Pfam; PF00628; PROSITE; PS0118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIAA1111 PROTEIN
                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                           EMBL; AB029034;
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99397452; PubMed=10470851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIAA1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel.
                                              83
                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                             67
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                                                                                                                                          seg
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                                                                                                                                                                                                                                                                                                                                             large proteins in vitro.";
Res. 6:197-205(1999).
L; AB029034; BAA83063.1; -.
erPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Similarity:
                                                                                          TyrCysLeuCysArgLeuProTyrAspValThrArgPheMetIleGluCy
                                                                                                                  TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAGGGCTGCACTGACTGG
                                            sAspMetCysGlnAspTrp
                                                                     CGAGGGCTGCACTGACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrCysLeuCysArgLeuProTyrAspValThrArgPheMetIleGluCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
                     sp_fungi:Q03012
                                                                                                                                          1/1 to:
                                                                                                                                                                                                                                                                                                 SM00249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                           00628; PHD; 1.
PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                   IPR000561; EGF-
IPR001965; PHD.
                                                                                                                                                                                                                                                                           1084
                                                                                                                                          Q9UPP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9НАН2
                                                                                                                                                                                                                                                                                               PHD;
                                                                                                                                                                                                                                                                          AA:
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4.625
69.565
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4.625
69.565
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Primates;
                                                                                                                                                                                                                                                                          120376 MW;
                                                                                                                                          from: 1
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13,
17,
                                              89
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Gaps: 0
Percent Identity: 43.478
                                                                                                                                                                                                    Percent
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Gaps: 0
Identity: 43.478
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RX MEDLINE-9731371; PubMed-9169875;
RX MEDLINE-9731371; PubMed-9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W.,
RA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,
RA Dowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,
RA Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,
RA Delius H., DiPaolo T., Dubois E., Dusterboft A., Duncan M., Floeth M.,
RA Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,
RA Heumann K., Hilbert H., Hiller L., Hunlcke-Smith S., Hyman R.,
RA Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D.,
RA Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,
RA Mewes H.W., Mirtipati S., Moestl D., Marathe R., Messenguy F.,
RA Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M.,
RA Nentwich U., Schafer M., Scharens B., Schramm S.,
RA Purnelle D., Schafer M., Scharens B., Schramm S.,
RA Vierendeer M., Sdiou A.M., Tettelin H., Urresterazu L.A., Ushinsky S.,
RA Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y.,
RA Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,
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Q03012;
Q1-NOV-1996
Q1-NOV-1996
                         SEQUENCE FROM N.A.
Swartzman E., Viswanathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                adrenoleukodystrophy gene.";
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95320205; PubMed=7597071;
Shani N., Watkins P.A., Valle D.;
"PXA1, a possible Saccharomyces cerevisiae ortholog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activated protein kinase-kinase homologs, mediated by protein kinase C."; Mol. Cell. Biol. 13:3076-3083(1993).
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Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93140769; PubMed=8423796;
Brigati C., Kurtz S., Balderes D., V
"An essential yeast gene encoding a
"An essential yeast gene encoding a
Mol. Cell. Biol. 13:1306-1314(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=90360986; PubMed=2167832;
Tzagoloff A., Capitanio N., Nobrega M.P., Gatti D.;
Tztochrome oxidase assembly in yeast requires the j
homolog of the P. denitrificans protein encoded by (
EMBO J. 9:2759-2764(1990).
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Jiang B., Brown J.L., Sheraton J., Fortin N., Bussey H.;
"A new family of yeast genes implicated in ergosterol synthesis is
related to the human oxysterol binding protein.";
yeast 10:341-353(1994).
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                                                                                "The nucleotide se
Nature 387:0-0(0).
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            E., Viswan
(APR-1996)
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
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., Lee K.S., Levin
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              the EMBI
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                                                                                                Saccharomyces cerevisiae
              .N., Emerick A.E., EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                92:6012-6016(1995).
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              Thorner J.; databases.
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ORF3.";
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alignment_scores:
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US-09-684-016-48411 x 074508
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Hall J., DePaulo T., A
Storms R.K., Vo D.H., I
Submitted (APR-1996) t
                                                                                                                  Rieger M., Lyne M., Rajandream M.A., Barrell B.G.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AL031523; CAA20664.1; ...
Interpro; IPR001065; PHD.
Pfam; PF00628; PHD; 1.
SMART; SM00249; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                         074508
074508;
                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TremBLrel. 08, Created)
01-NOV-1998 (TremBLrel. 08, Last sequence update)
01-UN-2001 (TremBLrel. 17, Last annotation update)
PUTATIVE TRANSCRIPTIONAL REGULATORY PROTEIN, PHD FINGER CONTAINING
                                                                                                                                                                                                                                                                                             SPCC594.05C
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Submitted (SEP-1997) to the
EMBL; 043703; AAB68222.1; -.
SGD; S0006059; YPL138C.
                                                                                                                                                                                               STRAIN-972H-;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 NCBI_TaxID=4896;
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AA; 41468 MW;
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O45410 PRELIMINARY;
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045410;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                  172 TyrCysValCysGlnLysProTyrAspAspThrLysPheTyrValGlyCy
                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00503; BROMODOMAIN.2; 1. PROSITE; PS50014; BROMODOMAIN.2; 1. PROSITE; PS01186; EGF_2; UNKNOWN_1.
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113 uGlyCysAspGlyCysGluAspTrp
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SMART; SM00249; PHD; 2.
SEQUENCE 405 AA; 46199
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InterPro; IPR000561; EGF-like.
InterPro; IPR001487; Bromodomain.
InterPro; IPR001965; PHD.
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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seq\_name:

sp\_invertebrate: Q9NLC1

PRT;

451

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sAspSerCysGlnGlyTrp 194

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. seq_documentation_block:
ID 045407 PRELIMINARY;
AC 045407;
DT 01-JUN-1998 (TrEMBLrel. 06,
DT 01-JUN-1998 (TrEMBLrel. 17,
DE 726H11.3B PROTEIN.
GN F26H11.3B.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoc
OC Rhabditidae; Peloderinae; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID Q9NLC1;
AC Q9NLC1;
DT Q1-CCT-2000 (TrEMBLrel. 15
DT Q1-CCT-2001 (TrEMBLrel. 15
DT Q1-CCT-2001 (TrEMBLrel. 17
DE F26H11.3C PROTEIN.
GN F26H11.3C PROTEIN.
GN F26H11.3C PROTEIN.
CO Eukaryota; Metazoa; Nematoo
CC Rhabditidae; Peloderinae; QC Eukaryota; Metazoa; Nematoo
CC Rhabditidae; Peloderinae; QC Rhabditidae; Peloderinae; QC NCBLTAXID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (NOV-1996) to the RN [2]
RN [2]
RN [2]
RN MEDLINE=99069613; PubMed=9, RA MEDLINE=99069613; PubMed=9, RA None; Sequence of the new rinvestigating biology "; RN [2]
RR InterPro; IPR001487; BGF0-1
DR InterPro; IPR001487; BGF0-1
DR InterPro; IPR001487; BGF0-1
DR Ffam; PF00628; PHD; 2.
DR PANRT; SM00297; BROMODOMA DR SMART; SM00297; BGF0-1
DR PROSITE; PS01186; EGF 2.
DR PROSITE; PS01014; BGMODOM
DR PROSITE; PS0104; BGF 2.
DR PROSITE; PS0104; BGF0-10
DR PROSITE; PS0104; BG
                                                                                                                                                                                                                                                                                                                                                           seq_name: sp_invertebrate:045407
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US-09-684-016-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-684-016-48411 x Q9NLC1
                                                                                         01-JUN-1998 (TIEMBLIEL 06, 01-JUN-1998 (TIEMBLIEL 06, 01-JUN-2001 (TIEMBLIEL 17, F26H11.3B PROTEIN. F26H11.3B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00503; BROMODOMAIN. SMART; SM00297; BROMO; 1. SMART; SM00249; PHD; 2.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
   Eukaryota; Metazoa; Nematoda; Rhabditidae; Peloderinae; Caer
                                                                                                                                                                                                                                                                                                                                                                                                                        234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50014; BROMODOMAIN_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
SEQUENCE 451 AA; 52035 MW; 349F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TremBLrel. 15, 01-OCT-2000 (TremBLrel. 15, 01-JUN-2001 (TremBLrel. 17, F26H11:3C PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 TyrCysValCysGlnLysProTyrAspAspThrLysPheTyrValGlyCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00439; bromodomain; 1. Pfam; PF00628; PHD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 282:2012-2018(1998).
EMBL; 281515; CAB54234.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                     sAspSerCysGlnGlyTrp 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
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IPR000561; EGF-like.
IPR001965; PHD.
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4.429
60.870
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   Dda; Chromadorea; Rhabditida; Rhabditoidea;
Caenorhabditis.
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                                                                                                                                                   Created)
Last sequential Last anno
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Last annotation update)
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: 0
: 34.783
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seq_documentation_block:
ID Q9UIG2
AC Q9UIG2;
AC Q9UIG2;
DT Q1-MAY-2000 (TrEMBLrel. 13
DT Q1-MAY-2000 (TrEMBLrel. 13
DT Q1-JUN-2001 (TrEMBLrel. 17
DE BROMODOMAIN PHD FINGER TRA
GN BPTF.
QS Homo sapiens (Human).
QC Eukaryota; Metazoa; Chorda
QC Eukaryota; Metazoa; Chorda
QC Mammalia; Eutheria; Primat.
QX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
Jones M.H., Hamana N., Shi
RA Jones M.H., Hamana Ocharc
RT Transcription factor.";
RL Submitted (SEP-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQUENCE PRODUCT OF THE PRODUCT OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                      SEQUENCE FROM N.A.
Jones M.H., Hamana N., Shimane M.;
Jones M.H., Hamana N., Shimane M.;
Tiedentification and charcterization BPTF a novel bromodomain transcription factor.";
                                                                                                                                                                                                                Homo sapiens (Human).
Homo sapiens (Human).
'~rvota; Metazoa; Chordata; '~rotia; Primates;
                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BROMODDOMAIN PHD FINGER TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 TyrCysValCysGlnLysProTyrAspAspThrLysPheTyrValGlyCy
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PROSITE; PS01014; BROMODOMAIN.2; 1.
PROSITE; PS01015; EGF_2; UNKNOWN_1.
SMART; SM00297; BROMO; 1.
SMART; SM00249; PHD; 2.
SEQUENCE 510 AA; 57880 MW; C567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00439; bromodomain; 1. Pfam; PF00628; PHD; 2.
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EMBL; Z81515; CAB04195.1; -.
InterPro; IPR000561; EGF-lik
InterPro; IPR001487; Bromodo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1996) to
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4.429
60.870
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          to the EMBL/GenBank/DDBJ databases
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Gaps: 0
Percent Identity: 34.783
                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C567A57D0DBE160F CRC64;
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Sequence of the sequence of th
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US-09-684-016-48411 x Q9UIG2
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Quality:
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EMBL; AF010404; AAC51735.1; -..

InterPro; IPR000910; HMG_12_box.

InterPro; IPR001214; SET.

InterPro; IPR00182; Recombinase.

InterPro; IPR001965; PHD.

InterPro; IPR002965; P_rich_extensn.
Pfam: PF00628; PHD; 3.
Pfam: PF00856; SET; 1.
PRINTS: PR01217; PRICHENTENSN.
PROSITE: PS00398; RECOMBINASES_2; UI
PROSITE: PS00398; SET; 2.
SMART: SM00541; FYRC; 1.
SMART; SM00541; FYRN; 1.
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O14687 PRELIMINARY;
O14687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2620
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                                                                                                                                                                         InterPro; IPR003616; PostSET.
InterPro; IPR003888; FYrich_N.
InterPro; IPR003889; FYrich_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=97388474; PubMed=9247308; Prasad R., Zhadanov A.B., Sedkov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00297; BROMO; 1.
SMART; SM00249; PHD; 2.
SEQUENCE 2781 AA; 311210 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS: PR00503; BROMODOMAIN.
PROSITE: PS00033; BROMODOMAIN.
PROSITE: PS50014; BROMODOMAIN. 2; 1.
PROSITE: PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB032251; BAA89208.1; ... Interpro; IPR000561; EGF-like. Interpro; IPR001487; Bromodomain. Interpro; IPR001485; PHD. Pfam; PF00439; bromodomain; 1. Pfam; PF00628; PHD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                         trithorax."
                                                                                                                                                                                                                                                                                                                                                                                                                                                              strong homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canaani E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rallapalli R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure and expression pattern strong homology to ALL-1 involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhadanov A.B., Sedkov Y., Bullrich F., Dru-R., Yano T., Alder H., Croce C.M., Huebner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.00
4.286
60.870
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17,
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Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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O:
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Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           human ALR, a no
acute leukemia
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on update)
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: 0
: 34.783
                                                                                                                                                                                                                                                                                                                                                                                                                                                              , a novel
kemia and
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bner K., M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene with
to Drosophila
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seq_documentation_block:
ID 014686
AC 014686;
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-JUN-2001 (TrEMBLrel. 17
DE ALR.

OS Homo sapiens (Human).
C Eukaryota; Metazoa; Chorda
OC Mammalia; Eutheria; Primat
OX NCBL_TAXID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97388474; PubMed-9
RA Allapalli R., Yano T., All
RA Canaani E.;
STUCTURE and expression |
RT Structure and expression |
RT STUCTURE and EXPRESSION |
RT STUCTURE and EXPRESSION |
RT INTEPPO; IPR001822; Recom
INTEPPO; IPR0019124; SET;
DR InterPro; IPR0019124; SET;
DR INTERPO; IPR001825; PLIC
DR INTERPO; IPR001825; PLIC
DR INTERPO; IPR001888; FYRIC
DR INTERPO; IPR00388; FYRIC
DR INTERPO; IPR00388; FYRIC
DR FAMT; SM00542; FYRC; 1.
DR SMART; SM00541; FYRN; 1.
DR SMART; SM00542; FYRC; 1.
DR SMART; SM00543; PDD; 7.
DR SMART; SM00541; FYRN; 1.
DR SMART; SM00541; FYRN; 1.
DR SMART; SM00542; FYRC; 3.
DR SMART; SM00543; PDD; 7.
DR SMART; SM00543; FYRC; 1.
DR SMART; SM00541; FYRN; 1.
DR SMART; SM00541; FYRN; 1.
DR SMART; SM00541; FYRN; 1.
DR SMART; SM00542; FYRC; 1.
DR SMART; SM00543; FYRC; 1.
DR SMART; SM00543; FYRC; 1.
DR SMART; SM00547; FYRN; 1.
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    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR DR DR SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: sp_human:014686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-97388474; PubMed=9247308;
Prasad R., Zhadanov A.B., Sedkov Y.,
Rallapalli R., Yano T., Alder H., Cro
Canaani E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
SMART;
SMART;
SMART;
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EMBL; AF010403; AAC51734.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  930 CysHisAlaProTyrValGluGluAspLeuLeuIleGlnCysArgHisCy
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SM00249;
SM00508;
SM00317;
VCE 4957
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                                                                                                                                                                                                                                                                                                                       IPR000910; HMG_12_box.
IPR001214; SET.
IPR001822; Recombinase
IPR001841; Znf_ring.
                                                                                                                                                                                                                                                 IPR003616; PostSET
                                                                                                                                                                                                                                                                                      IPR001965; PHD.
IPR002965; P_rich_extensn
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PHD; 4.
POSTSET; 1.
SET; 1.
AA; 531848
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4.615
65.000
                                                                                                                                                                                   PRICHEXTENSN
                                                                                                                                              RECOMBINASES_2;
SET; 2.
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Primates;
                                                                                                                                                                                                                                   FYrich_N. FYrich_C.
     1.
564181 MW;
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05,
17,
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Last annotation updat
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       26B7C74CAD417E44 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  of human ALR, a no
in acute leukemia
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Croce C.M.,
                                                                                                                                                                 UNKNOWN_1.
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45.000
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Huebner K., Mazo A.,
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seq_documentation_block:
ID 022662:
PRELIMINA
AC 022662:
PT 01-NOV-1996 (TYEMBLIE
DT 01-NOV-1996 (TYEMBLIE
DT 01-JUN-2001 (TYEMBLIE
DE T22C1.1
OS Caenorhabditis elegar
OC ELMATYOLE: Metazoa; h
OC Rhabditidae; Peloderi
OX NCBI_TAXID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RA MCMULTAY A.;
RL SUDMITTED (JUN-1996)
RN SEQUENCE FROM N.A.
RA MCMULTAY A.;
RA MEDLINE=94150718; Pul
RA MISON R., AINSCOUGH
RA HONFIELD J., BUTTON N.
RA CITAXTON M., DEUTON N.
RA Gardner A., Green P.
RA JONES M., Kershaw J.
RA JONES M., Kershaw J.
RA JONES M., Sershaw J.
RA Lightning J., Lloyd (RA PATSONS J. PETCY C.
RA Thierry-Mieg J., Thool
RA Watson A., Weinstock
RT elegans ";
RL Nature 368:32-38(199)
DR EMBL; Z75550; CAA999
DR INTERPO2207; Zf-UB
DR SMART; SM00396; ZnF_
SEQUENCE 416 AA;
                                                                                                                                 alignment_block:
US-09-684-016-48411 x Q22662
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US-09-684-016-48411 x O14686
                                                                                                                                                                                                                                                                        alignment_scores:
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                                                                                         Align seg 1/1 to: Q22662
                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: 014686 from: 1
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                                                                                                                                                                                                                                                                                                                                        Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Coolson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1235 CyshisAlaProTyrValGluGluAspLeuLleGlnCysArgHisCy 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 CACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                            AGGTATTGTAAATGTGAGATGCCTTACAACCCTGATGAC......CT
LysPheCysThrCysAspValPheTyrProAspGluAspGlyGlyLysGl 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sGluArgTrp 1254
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                                                                                                                                                                                                                                                   Quality:
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3.719
59.259
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4.615
65.000
                                                                                         from: 1
                                                                                                                                                           Percent Identity: 37.037
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Gaps: 0
Identity: 45.000
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seq_documentation_block:
ID Q970Al;
AC Q970Al;
AC Q970Al;
DT Q1-MAY-2000 (TrEMBLrel. 13
DT Q1-MAY-2001 (TrEMBLrel. 13)
DT Q1-MAY-2001 (TrEMBLrel. 13)
DT Q1-JUN-2001 (TrEMBLrel. 13)
DT Q1-JUN-2001 (TrEMBLrel. 13)
DT Q1-JUN-2001 (TrEMBLrel. 17)
DE HYPOTHETICAL 49.7 KDA PROT
GN T32AlG.30 OR AT4C33860.
OS Arabldopsis thaliana (Mous
OC Eurosids II; Brassicales;
OX Spermatophyta; Magnoliophy
OC eurosids II; Brassicales;
OX NCBL_TAXID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Zimmermann W., G
RA Mewes H.W., Mayer K.F.X.,
RL Submitted (MAY-1999) to th
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arrabidopsis sequencing
RL Submitted (MAY-1999) to th
RN [3]
RP SEQUENCE FROM N.A.
RA Zimmermann W., Grueneisen
RA EU Arrabidopsis sequencing
RA EU Arrabidopsis CABB1304.1
DR InterPro; IPR001955; PHD.
DR Pfam; PF002207; zf UBR1; 1.
DR Pfam; PF002207; zf UBR1; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00249; A43 AA; 49704.
seq_documentation_block:
ID Q9VRV6 PRELIMI
AC Q9VRV6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-684-016-48411 x Q9T0A1
                                                                                                                                                                           seq_name: sp_invertebrate:Q9VRV6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: sp_plant:Q9T0A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: Q9TOA1 from: 1 to: 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9TOA1;
Q9TOA1;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 13, Created)
Q1-JUN-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 13, Last sequence update)

                                                                                                                                                                                                                                                                                                                                                                                                                                            128 TyrCysThrCysAspArgProTyr...ProAspProAsnValGluGluGl 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00249; PHD; 1.
SMART; SM00396; ZnF_UBR1; 1.
Hypothetical protein.
SEQUENCE 443 AA; 49704 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/G
EMBL; ALO78468; CAB43886.1; -.
EMBL; AL161560; CAB81304.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P., Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                     143 nValGluMetIleGlnCysCysLeuCysGluAspTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001965; PHD.
InterPro; IPR003126; ZnF_UBR1.
Pfam; PF00628; PHD; 1.
Pfam; PF02207; zf-UBR1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 uLeuLeuGlnCysGluIleCysGluAspTrp 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 AATGGCGCAATGCGAGGGCTGCACTGACTGG
::: ||||||||||
                                                                                                                                                                                                                                                                                                                                                      41 .... CTAATGGCGCAATGCGAGGGCTGCACTGACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.50
4.250
48.276
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Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7DA998CA6ED2904D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73
                                                 662
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                                                                                                                                                                                                                                                                          155
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2
44.828
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alignment_block:
US-09-684-016-48411/rev
                                                                                                                    alignment_scores:
                                                                                                                                                                                 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell N.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berovva D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
RA Burtts K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtts K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriera S., Pleisohmann W.,
Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Glodek A., Gong F., Keft C., Kravitz S., Fleisohmann W.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lang Y., Lii X.,
Alasko P., Lei Y., Levitsky A.A., Li J.-Li Z., Liang Y., Lia X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., Moylanders R., Vuncoy D.M., Nechon D.L.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Noshrefi A.,
RA Mount S.M., Moylanders R., Vuncoy D.M., Nechon D.L.,
RA Kimmel R.E., Spradding A.C., Stapleton M., Skipski M.P., Smith T.,
RA Spier E., Spraddin
                                                             Percent Similarity:
                                                                                                                                                                          PROSITE; PS00028; ZINC_FINGER_C2H2_1; 10.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 11.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 662 AA; 76582 Mm. Cennon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000
01-MAY-2000
01-JUN-2001
CG7386 PROTE
CG7386.
                                                                                                                                                                                                                                                                                InterPro; IPR000822; znf-C2H2.
InterPro; IPR000130; zn_MTpeptdse.
Pfam; PF00096; zf-C2H2; 12.
SMART; SM00355; ZnF_C2H2; 12.
                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0035691; CG7386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                           Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 (TrEMBLrel.
0 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophilidae; Drosophila.
                                                        57.50
2.212
78.788
x Q9VRV6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13, Created)13, Last sequence update)17, Last annotation updat
                                                             Percent Identity:
                                                                                                                                                                                 258BE838CF67A8E9 CRC64;
                                                        33
1
36.364
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seq_documentation_block:
ID Q9BQW0 PRELIMINARY;
AC Q9BQW0,
DT 01-JUN-2001 (TrEMBLrel. 17
DT 01-JUN-2001 (TrEMBLrel. 17
DT 01-JUN-2001 (TrEMBLrel. 17
DT 01-JUN-2001 (TREMBLRel. 17
DT 01-JUN-2001 (TREMBLRel. 17)
DE DJ885L7.9.3 (DEATH ASSOCIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-684-016-48411 x Q9UT79
                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
   Quality:
                                                                                                                               seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: sp_fungi:Q9UT79
                                                                                                                                                                                                                                                                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                1457 CysLeuCysArgGlnProPheAlaIleSerAspGlyThrValGlnCysHi 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murphy L., Harris D., Wood V., Rajandream M.A., Barrell Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases EMBL; AL109739; CAB52274.1; -. Interpro; IPR000345; CytC_heme_bind. Interpro; IPR000561; EGF-like. Interpro; IPR001965; PHD. Interpro; IPR001965; PHD. Interpro; IPR003347; JmjC. Interpro; IPR003347; JmjC. Interpro; IPR003349; JmjN. Pfam; PF00628; PHD; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSUT79 PRELIMINARY; PRT; 1588 AA.
OSUT79;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIYE TRANSCRIPTIONAL REGULATORY PROTEIN, PHD FINGER.
SPAC343.11C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS01180; EGF_2; UNKNOWN_1.
SMART; SM00249; PHD; 3.
SMART; SM00249; PHD; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomycetales;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=972H-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 LeuValPheSerArgLeuArgLeu...LeuThrIleHisLeuLysLysVa 279
                                                                                                                                                                                                  58
                                                                                                                                                                                                                                                                  œ
                                                                                                                                                                sAsnCysLeuGluTrp
                                                                                                                                                                                                GGGCTGCACTGACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGTCAGTGCAGCCCTCGCATTGCGCCCATTAGGTCATCAGGGTTGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGTGTGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTAC 73
                                                                                                                               sp_human:Q9BQW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF02373;
                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1588
 (TYEMBLrel. 17, Created)
(TYEMBLrel. 17, Last sequence update)
(TYEMBLrel. 17, Last annotation updat
(DEATH ASSOCIATED TRANSCRIPTION FACTO
                                                                                                                                                                                                                                                                                                 Q9UT79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        jmjc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHD;
AA;
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                                                                                                                                                                                                                                                                                                                                                                              57.00
3.562
72.727
                                                                                                                                                                   1478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180350 MW;
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Ö:
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6
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                                                                                                                                                                                                                                                                                                 1588
                                                                                   379
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 update)
FACTOR 1
                                                                                                                                                                                                                                                                                                                                                                               22
0
36.364
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   (CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
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SQ
                                                                                                                                        alignment_block:
US-09-684-016-48411 x Q9BW03
                                                                                                                                                                                                                alignment_scores:
Quality:
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US-09-684-016-48411 x Q9BQW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: sp_human:Q9BW03
                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: Q9BQW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    documentation_block:
                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
EMBL; BC000770; AAH00770.1; -.
Hypothetical protein.
SEQUENCE 544 AA; 59487 MW; 193341A77ED5FAL
                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 59.5 KDA PROTEIN.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                     270 TyrCysIleCysArgGlnProHisAsn...AsnArgPheMetIleCysCy
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=KIDNEY ADENOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BW03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9BW03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2001) to the EMBL; AL035669; CAC28883.1; NON_TER 1
285 sAspArgCysGluGluTrp 291
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 379 AA; 41245 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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                                                                                                                seg 1/1 to:
                         CGAGGGCTGCACTGACTGG
                                                                                   TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                Q9BW03 from: 1
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3.531
69.565
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Gaps: 1
Percent Identity: 39.130
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                                                                                                                                                                                                                                                                         193341A77ED5FADA CRC64;
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    Quality:
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RA ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Irakawa K., Ono Y., Takiguchi S.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
"MEDO human cDNA sequencing project.";
"INEDO human cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: Q9NUM8 from: 1
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TISSUE-COLON ADENOCARCINOMA;
Strausberg R.;
Submitted (MAR-2001) to the EMB
EMBL; BC004237; AAH04237.1; -.
Hypothetical protein.
SEQUENCE 562 AA; 61353 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _documentation_block:
Q9BTC0 PRELIMINARY;
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                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 61.4 KDA PROTEIN.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat;
Eukaryota; Metazoa; Primates; Catarrhini; Hominid
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Q9NUMB;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CDNA FLJ11265 FIS, CLONE PLACE1009158.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9BTC0;
                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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     91A714668F9C5C12
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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
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                                                                                                                     seq_name:
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US-09-684-016-48411 x Q9WV00
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US-09-684-016-48411 x Q9BTC0
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    Q9WV00 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misexpression disrupts limb development.";
Proc. Natl. Acad. Sci. U.S.A. 96:7992-7997(1999).
EMBL; AJ238332; CAB48401.1;
MGD; MGI:1344352; Dido1.
InterPro; IPR001965; PHD.
Pfam; PF00628; PHD; 1.
SMART; SM00249; PHD; 1.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
DEATH INDUCER-OBLITERATOR-1 (FRAGMENT).
DIDO1 OR DIO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIJINE-93324176; PubMed=10393935;

Garcia-Domingo D., Leonardo E., Grandien A., Martinez P., Izpisua-Belmonte J.C., Martinez-A C.;

"DIO-1 is a gene involved in onset of apoptosis in vitro,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                   267
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                              PRELIMINARY;
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seq_documentation_block:
ID 015043;
AC 015043;
AC 015043;
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-JAN-1998 (TrEMBLrel. 17
DE KIAA0333 (FRAGMENY).

GN KIAA0333 (FRAGMENY).

CC Eukaryota; Metazoa; Chorda
OC Eukaryota; Metazoa; Chorda
OC Mammalia; Eutheria; Primat
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.

FROUENCE FROM N.A.

ROBI_TaxID=984; PubMed=9
RA Magase T., Ishikawa K., Na
RA Tanaka A., Kotani H., Nomu
RT "Prediction of the coding;
RT The complete sequences of
RT The complete sequences of
RT Code for large proteins in
RL DNA Res. 4:141-150(1997).
DR EMBL; AB003331; BAA20791.1
DR InterPro; IPR001052; Rubre
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InterPro; IPRO0160; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOm; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
SEQUENCE 641 AA; 71090 MW;
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01-NOV-1999
01-JUN-2001
P73.
                                                          Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
"Fish p73, ancestoral p53?";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF043641; AAD27752.1; -.
HSSP; O15350; ICCK.
                                          code for large proteins in vitro. DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human).

Craniata; Vertebrata;

Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   520 .......GlyLeuGlnSerValTyrHisLeuGln 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487 HisCysThrProProProProTyrAsnProAspProSerLeuValSerPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata
Actinopterygii; Neopterygii; Teleostei
Cypriniformes; Cyprinidae; Cyprininae;
                                                                                                                                                            MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             503 eLeuThrSerLeuGlyCysGlnAsnCysIleAspTyrPheThrSerGln.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barbus barbus (Barbel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=40830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 TAAGGTGATACTTATCTTCAATTTATTCCACACAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAA...:::||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ......TGCGAGGGCTGCACTGACTGGTAAGTTTCACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_human:015043
                        AB002331; BAA20791.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9W664 from: 1
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2.260
55.556
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05,
17,
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                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Craniata;
Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4A215B21AEB16E4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641
                                                                                                                                                                                                                                                                                                                                                                                                                                       991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
Euteleostei; Ostariophysi
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45
2
31.111
                                                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519
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seq_documentation_block:
ID Q944G6
AC Q944G6
DT Q1-MAR-2001 (TrEMBLTE
DT Q1-MAR-2001 (TrEMBLTE
DT Q1-JUN-2001 (CONTAINS K
GN DJ85L7-9.1 (CONTAINS K
GN DJ85L7-9.1 (CONTAINS K
GN DJ85L7-9.1
COMAMMALIA; EUTHAND).
OC EUKARYOTA; Metazoa; C
OC Mammalia; EUTHAND).
OC EUKARYOTA; Metazoa; C
OC Mammalia; EUTHAND).
OR CONTAINS (HUMAN).
RA SMATH M.;
RA SMITH M.;
RA SMART; SMO01965;
DR INTERPOO1209;
DR SMART; SMO0249; PHD; 1
DR SMART; SMO0249; PHD; 1
DR SMART; SMO0510; TF52M
DR PROSITE; PS0527; RIB
FT NON_TER
SQ SEQUENCE 1042 AA;
                                                                                                                                                                      alignment_scores:
    Quality:
    Ratio:
                                                                                           alignment_block:
US-09-684-016-48411 x Q9H4G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
                                                        Align seg 1/1 to: Q9H4G6 from: 1
                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: 015043 from: 1
                                                                                                                                                                                                                                                                                                     Submitted (OCT-2000) to the EMBL/GenBank/DDBJ date EMBL; AL035669; CAC12756.1; -.

InterPro; IPR001965; PHD.

InterPro; IPR001269; RLbosomal_S14.

InterPro; IPR003618; TFS2_cent.

Pfam; PF00628; PHD; 1.

SMART; SM00249; PHD; 1.

SMART; SM00249; PHD; 1.

SMART; SM002510; TFS2M; 1.

PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-684-016-48411 x 015043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DJ885L7.9.1 (NOVEL PROTEIN SIMILAR TO MOUSE DEATH INDUCER OBLITERATOR
1 (DIO-1) (CONTAINS KIAA0333) (ISOFORM 1)) (FRAGMENT).
DJ885L7.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0163; RÜBREDOXIN.
PROSTIE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
SMART; SM00249; PHD: 1.
SMART; SM00510; TFS2M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00628; PHD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001209; Ribosomal_S14
InterPro; IPR001965; PHD.
InterPro; IPR003618; TFS2_cent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36
                TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrCysIleCysArgGlnProHisAsn...AsnArgPheMetIleCysCy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
  Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
56.50
3.531
69.565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.50
3.531
69.565
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107368
                                                                                                                                                                                                                                                                       112916 MW;
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                                                                                                                                                     Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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5
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                                                                                                                                                                                                                                                                       F1ADB40059F09742 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identity: 39.130
                                                        1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1042 AA
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1
39.130
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                  54
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Sequence of the sequence of th
alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: Q9YEG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-684-016-48411/rev x Q9YEG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.
A Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kost
A Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
A Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
A Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
A Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
T "Complete genome sequence of an aerobic hyper-thermophilic
Crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
R EMBL; Ap000060; BAA79594.1; --
CRENDITE; PS00213; LIPOCALIN; UNKNOWN_1.
R FORSITE; PS00213; LIPOCALIN; UNKNOWN_1.
W Hypothetical protein; Complete proteome.
Q SEQUENCE 544 AA; 55839 MW; 14028D4D558A7891 CRC64;
                                                                                                                                                                                                                                                                                                                                        documentation_block:
Q9RLR4 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
                                                                                                                                                                                                       Q9RLR4 PRELIMINARY;
Q9RLR4;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAR-2001 (TrEMBLrel. 16,
                      Legionella pneumophila.
Bacteria; Proteobacteria;
Legionellaceae; Legionella
NCBI_TaxID=446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9YEG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 rCysSerProArgIleAlaAlaLeuGly 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 TrpGluProIleAspAlaValPheLysValGluIleGluLeuAspArgSe 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 TGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTACCAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation updat)
HYPOTHETICAL 55.8 KDA PROTEIN APE0614.
                                                                                                                                                       LVHB10.
                                                                                                                                                                                 LVHB10 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=K)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=56636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aeropyrum pernix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APE0614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 GTGCAGCCCTCGCATTGCGCCATTAGGT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 TyrCysIleCysArgGlnProHisAsn...AsnArgPheMetIleCysCy 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                          Legionella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.00
3.111
69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to:
                                                                                       gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity:
                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                          subdivision; Legionellaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                        363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
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0
38.462
                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haikawa Y.,
ai A., Kosugi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                л H.,
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                                                                                   group;
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seq_name: sp_human:Q9NR48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-016-48411/rev x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
           Pfam; PF01426; BAH; 1.
Pfam; PF00439; bromodomain; 1.
Pfam; PF00628; PHD; 1.
Pfam; PF00856; SET; 1.
SMART; SM00384; AT hook; 3.
SMART; SM00439; BAH; 1.
SMART; SM00297; BROWO; 1.
SMART; SM00297; BROWO; 1.
SMART; SM00210; PHD; 1.
SMART; SM00508; POStSET; 1.
SMART; SM00317; SET; 1.
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Q9NR48 PRELIMINARY;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDILINE-20319018; PubMed=10860993;

MEDILINE-20319018 J., Tada S., Rozovskaia T.,

Nakamura T., Blechman J., Tada S., Rozovskaia T.,

Bullrich F., Mazo A., Croce C.M., Geiger B., Cana

"huASH1 protein, a putative transcription factor

homologue of the Drosophila ash1 gene, localizes

cell-cell tight junctions.",

Proc. Natl. Acad. Sci. U.S.A. 97:7284-7289(2000).

EMBL; AF257305; AAF68983.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20032053; PubMed-10564519; Segal G., Russo J.J., Shuman H.A.; Relationships between a new type-IV secretion virulence system of Legionella pneumophila."; Mol. Microbiol. 34:799-809(1999).

EMBL; Y19029; CAB60060.1; -. SEQUENCE 363 AA; 39117 MW; F23E77A30A279BC7
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                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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STRAIN-PHILADELPHIA-1;
                                                                                                                                                         InterPro; IPR003616; PostSET.
InterPro; IPR001214; SET.
                                                                                                                                                                                    InterPro; IPR000637; AT_hook.
InterPro; IPR001025; BAH.
InterPro; IPR001487; Bromodomain.
InterPro; IPR001965; PHD.
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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2.220
67.568
BROMODOMAIN_2;
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Last sequence update)
Last annotation updat
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seq_documentation_block:
ID Q9HOS7
AC Q9HOS7,
C Q9HOS7,
DT Q1-MAR-2001 (TrEMBLrel. 16
DT Q1-MAR-2001 (TrEMBLrel. 16
DT Q1-JUN-2001 (TrEMBLrel. 16
DT Q1-JUN-2001 (TrEMBLrel. 17
DE HYPOTHETICAL 20.3 KDA PROT
GN DKFZP564J1864.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chorda
OC Mammalla; Eutheria; Primat
OX NCBL_TaxID=9606;
RN [1]
RA Duesterhoeft A., Lauber J.
RL Submitted (JAN-2000) to th
DR EMBL; AL136660; CAB66595.1
DR InterPro; IPRO00531; TONB_DEF
KW Hypothetical protein.
SQ SEQUENCE 180 AA; 20253
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US-09-684-016-48411 x Q9H0S7
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seq_name: sp_invertebrate:Q9XWD7
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                                                                        111 ATTCCACACAA 121
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PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 180 AA; 20253 MW; DB8008E0F3F6CDB0 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN,
Duesterhoeft A., Lauber J., Mewes H.W., Gassenhuber J.,
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL136660; CAB66595.1; -.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 20.3 KDA PROTEIN.
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                                                                                                            76 nIlePheAspTrpAsnValLysGlnLeuPheLeuTyrLeuSerAlaGluT
                                                                                                                                                  61 CTGCACTGACTGGTAAGTTTCACATGTAAGGTGATACTTATCTTCAATTT 110
                                                                                                                                                                                      60 ArgSerAspLeuGlyPheIleThrSerAspIleThrAlaAspLeuGluAs
                                                                                                                                                                                                                        11 AAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGAGGG
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                                       yrSerThrLys
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A; 332765 MW;
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alignment_scores:
Quality:
Ratio:
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RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Wilson R., Ainscough R., Connell M., Copsey T., Cooper J., Coulson A.,
RA Graxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
RA Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA Smaldon N., Smith A., Sonnhammer E., Staden R., Waterston R.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
T. Telegans.",
T. Network C. Staden R., Sulston P.;
T. Network C. Staden R., Sulston P.;
T. Network C. Staden R., Weinston R.,
T. Telegans.",
T. Network C. Staden R., Weinston R.,
T. Network C. Staden R.,
                                                                                                                                                                                                                                                                                                                                                      seq_name: sp_plant:Q9FNI5
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US-09-684-016-48411/rev x Q9XWD7
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01-JUN-2001 (Tr
GB|AAC80581.1.
                                                                                                                                                                                                                                                                                                          documentation_block:
                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core «
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                          Q9FNI5;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                 175
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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01-NOV-1999 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
Y47H9C.2 PROTEIN.
STRAIN-COLUMBIA;
                    SEQUENCE FROM N.A.
                                                                NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGCCCTCGCATTGCGCCATT
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US-09-684-016-48411 x Q9FNI5
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InterPro; IPR001965; PHD.
Pfam; PF00628; PHD; 2.
SMART; SM00249; PHD; 3.
PROSITE; PS00018; EF_HAND; UNK
SEQUENCE 1516 AA; 170012 MW
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                                                                                                                                                                                                                                                                      investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL132952; CAB63382.1;
InterPro; IPR001214; SET.
InterPro; IPR001955; PHD.
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Q9U263;
Q9U263;
Q1-MAY-2000 (TrEMBLrel. 13,
O1-MAY-2000 (TrEMBLrel. 13,
O1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                 Pfam; PF00628; PHD; 1.
Pfam; PF00856; SET; 1.
PROSITE; PS50280; SET; 1.
                                                                                                                          SMART; SM00249; PHD;
SMART; SM00317; SET;
SEQUENCE 1645 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
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DNA Res. 4:291-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sulston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                        none;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Sulston J.E.;
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a; 170012 MW; FFAAA8593BA93CEA CRC64;
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                                                                                                                               74BF8830788BED57 CRC64;
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Gaps:
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O44498 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Coolson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortinore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
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                                                                                                                                                                                                                         PROSITE; PS50280; SET; 1.
SMART; SM00249; PHD; 1.
SMART; SM00317; SET; 1.
SEQUENCE 1655 AA; 1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
Submitted (DEC-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Miller N., Stellyes L.,
Submitted (DEC-1997) to
                                                                                                                                                                                                                                                                                                                                        Pfam; PF00628; PHD; 1.
Pfam; PF00856; SET; 1.
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InterPro; IPR001214; SET.
InterPro; IPR001965; PHD.
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MEDLINE=94150718; PubMed=7906398;
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Eukaryota, Metazoa, Ner
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182580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L., Bradshaw H., Keppler D.;
to the EMBL/GenBank/DDBJ databases
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RA Adams M.D., Celniker S.E., Holt R.A., K., Kabhurner M., Galle R.F.,
RA Adams M.D., Celniker S.E., Holt R.A., Kabhurner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Pleischman W.,
ROSING C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Clodek A., Gong F., Gorrell J.H., Gu Z., Gana P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Ra Hasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Ra Harris M., Wobart S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Ra Harris M., Wobart S., Sanders R., Diac M., Wang X.,
Ra Ra Harris M., N
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01-JUN-2001 (TrEM
CG15637 PROTEIN.
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Q9VR08;
01-MAY-2000
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                                                                   EMBL; AE003576; AAF51000.1; HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                     FlyBase; FBgn0000488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   821 CysHisCysGlyMetAspHisGlyAspGlyAspThrIle...GluCysGl 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGCTGCACTGACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 044498 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
Asx_hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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6
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InterPro; InterPro;

; IPR002899; ; IPR000561;

InterPro;

EGF\_Ca. EGF-like.

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seq_documentation_block:
ID Q9V7S1;
AC Q9V7S1;
DT 01-MAY-2000 (TrEMBLEG
DE CG5065 PROTEIN.
GN CG5065.
OC ELWARYOTA; Metazoa; A
OC Pterygota; Neoptera;
OC Ephydroidea; Drosophi
OX NCBI_TAXID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE-20196006; Pub
RA Adams M.D., Celniker
RA Berorge R.A., Lewis S.,
RA Sutton G.G., Wortman
RA Burtin G.G., Wortman
RA Burtin G.G., Wortman
RA Ballew R.M., Basu A.,
RA Beeson K.H., Doyle C., I
RA Beeson K.J., Busam D.,
RA Burtis K.C., Busam D.,
RA Cherry J.M., Cawley S
RA Godson K., Doup L.E.,
RA Durbin K.J., Evangeli
RA Durbin K.J., Evangeli
RA Glodek A., Gong F., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
Ratio:
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US-09-684-016-48411 x Q9VR08
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An Annatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
An Annatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
An George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
An Helt G., Nelson C.R., Miklos G.L.G.,
An Helt G., Nelson C.R., Miklos G.L.G.,
An Henderson S.N., Miklos G.L.G.,
Andril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
An Henderson K.Y., Benos P.V., Berman B.P., Bhandari D., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
An Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
An Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
An Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
An Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
An Borkova D., Botchan M.R., Bouck J., Bovenport L.B., Davies P.,
An Borkova D., Delcher A., Delng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Cawley S., Dahlke C., Davenport L.B., Davies P.,
An Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
An Dordon K.J., Evangelista C.C., Ferriac S., Fleischmann W.,
An Fosler C., Gaptiellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
An Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q9VR08
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ProDom; PF0003573; ET; 1.
SMART; SM00179; EGF_CA; 16.
SMART; SM00019; EGF_Like; 35.
SMART; SM00209; WR1; 5.
SMART; SM00289; WR1; 2.
PROSITE; PS001010; ASX_HYDROXYL; 18.
PROSITE; PS001186; EGF_1; 1.
PROSITE; PS01186; EGF_2; 18.
PROSITE; PS01187; EGF_CA; 17.
Calcium-binding; EGF-Like domain; G1
SEQUENCE 3680 AA; 388637 MW; E5E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropóda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
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; IPR002603;
; IPR003645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
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3.633
62.500
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13,
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E5E972E1A3479EFF CRC64;
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alignment_block:
US-09-684-016-48411 x Q9V7S1
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    Quality:
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Molson D.R., Melson D.R., McHon R.N., Navoris J., Moshrefi A., Melson D.R., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Wenter E., Wang A.H., Wang X.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F. N., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
EMBL; AE003806; AAF57974 1: -
DR EMBL; AE003806; AAF57974 1: -
DR EMBL; AE003806; AS, 69682 MW; 8C12CD780F96D5E0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
FlyBase; FBgn0003044; Pcl.
InterPro; IPR001965; PHD.
InterPro; IPR002999; Tudor
                                                                                                                                                                                             melanogaster, a trans-acting
expression.";
                                                                                                                                                                                                                     Lonie A., D'andrea R., Paro R., Saint R.; "Molecular characterisation of the Polycomblike melanogaster, a trans-acting negative regulator
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ISOGENIC CHROMOSOME
                                                                                                EMBL;
                                                                                                                               Development 120:2629-2636(1994)
                                                                                                                                                                                                                                                                                                                             MEDLINE=95044940; PubMed=7956837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286
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                                                                                             -!- SIMILARITY: CONTAINS :
EMBL; L35153; AAA64457.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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3.857
56.000
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                                                                                                                                      PHD-FINGER DOMAINS
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RX MEDLINE-20196006; PubMed-10731132;

RX MEDLINE-20196006; PubMed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Burandon R.C., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: sp_invertebrate:Q9V8C2
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Quality:
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DNAIN 242 256
DOMAIN 274 277
DOMAIN 327 341 PO
DOMAIN 408 411 PO
DOMAIN 424 472 PO
DOMAIN 512 566 PO
DOMAIN 843 846
SEQUENCE 857 AA; 95289 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9V8C2; PRELIMINARY;
Q9V8C2; O1-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
PCL PROTEIN.
PCL OR CG5109.
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O9V8C2 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00628; PHD; 2.
SMART; SM00249; PHD; 2.
SMART; SM00333; TUDOR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrCysTyrCysGlyLysProGlyLysPheAspHisAsnMetLeuGlnCy
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Gaps: 0
Percent Identity: 43.478
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Last annotation update)
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POLY-PRO.
POLY-GLY.
PHD-FINGER.
PHD-FINGER.
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seq_documentation_block:
ID Q9FK65;
AC Q9FK65;
AC Q9FK65;
AC Q1-MAR-2001 (TrEMBLrel. 16
DT Q1-MAR-2001 (TrEMBLrel. 16
DT Q1-JUN-2001 (TrEMBLrel. 16
DT Q1-JUN-2001 (TrEMBLrel. 17
DE RECEPTOR-LIKE PROTEIN KINA
OS Arabidopsis thaliana (Mous
OC Eukaryota; Viridiplantae;
OC Spermatcophyta; Magnoliophy
OC eurosids II, Brassicales;
OX NCBI_TAXID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE-98403884; PubMed=9
RA Tabata S.;
RT "Structural analysis of Ar
RT Tabata S.;
RT Sequence features of the r
RT FINAL RT SEQUENCE TOWN
RT STAN RT SEQUENCE TOWN
RT STAN RT SEQUENCE TOWN
RT STAN RT
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-016-48411 x Q9V8C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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BYBLI, AE003800; AAF57748.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RECEPTOR-LIKE PROTEIN KINASE.
Arabidopsis thaliana (Mouse-ear Cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                             physically assigned P1 and TAC DNA Res. 5:203-216(1998). EMBL; AB012245; BAB09221.1; -.
                                                                                                                                                                                                                                                                                                        MEDLINE=98403884; PubMed=9734815;
Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
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SMART; SM00249; PHD; 2.
SMART; SM00333; TUDOR; 1.
SEQUENCE 1042 AA; 114506
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InterPro; IPR001965; PHD.
InterPro; IPR002999; Tudor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPhers Merkulov G., Milshina N.V., Mobarry C., Morris J., Mos Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M.,
                                                                                                                                                                                                                              Sequence features of the regions
                                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana of Sequence features of the regions of 1,367,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 CGAGGGCTGCACTGACTGG
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Gaps:
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InterPro; IPR001245; Tyr\_k pfam; PF00560; LRR; 2. Pfam; PF00069; pkinase; 1.

Tyr\_kin.

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seq_documentation_block:
ID 09VG78
AC 09VG78;
DT 01-MAY-2000 (TrEMBLTE
DT 01-MAY-2001 (TrEMBLTE
DT 01-JUN-2001 (TrEMBLTE
DT 01-JUN-2001 (TrEMBLTE
DE CG6525 PROTEIN.
GN CG6525.
OS Drosophila melanogast
OC Eukaryota; Metazoa; &
OC Ephydroidea; Drosophi
OX NCBI_TaxID-7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE-20196006; Pul
RA Adams M.D., Celniker
RA Adams M.D., Celniker
RA Adams M.D., Celniker
RA George R.A., Lewis S.
RA Sutton G.G., Wortman
RA Brandon R.C., Rogers
RA Barandon R.C., Rogers
RA Barandon R.C., Busuan D
RA Ballew R.M., Basu A.,
RA Beeson K.H., Doyle C., i
RA Ballew R.M., Basu A.,
RA Beeson K.G., Busam D
RA Cherry J.M., Cawley:
RA Dodson K., Doup L.E.
RA Durbin K.J., Delchel
RA Glodek A., Gong F., (
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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US-09-684-016-48411/rev x Q9FK65
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Quality:
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PRINTS; PRO0109; TYRKINASE.
SMART; SM00370; LRR; 4.
SMART; SM00221; SYYKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYYKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006; PubMed=10731132;
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 570 AA; 63537 MW; 972414BDE3A8DBC0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAACTTACCAGTCAGTGCAGCCCTCGCATTGCGCCATTAGGTCATCAGG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TrpAsnArg...ArgIleSerIleAlaLeuGlyAlaAlaArgGlyLeuVa
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Gaps: 3
Identity: 40.000
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US-09-684-016-48411 x Q9VG78
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   Quality:
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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Williams S.M., Wooddage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Williams S.M., Wooddage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Williams S.M., Zhong F.N., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Yeb T., Zhong F.N., Rubin G.M., Venter J.C.,

"The genome sequence of Drosophila melanogaster.";

RI Science 287:2185-2195(2000).

DR EMBL; AE003695; AAF54807.1;

DR EMBL; AE003695; AAF54807.1;

DR EMBL; CG5525.
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                                                                                                                                                                                                                                                                                                                                              documentation_block:
                                                                                                                                                                   Viruses; Retroid viruses; Retroviridae; RCBI_TaxID=11676;
                                                                                                                                                                                                                                                         01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                            Q98VX5;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                  927 sAspLeuCysGluAspTrp
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SMART; SM00510; TFS2M; 1.
SEQUENCE 2016 AA; 221998
                 NON_TER
                                                Mandal D., Chakrabarti S.;
"Divergent HIV-1 C subtypes
Submitted (MAR-2001) to the
EMBL; AJ311641; CAC34551.1;
                                                                                                                                                                                                                                         ENVELOPE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                               Q98VX5
 SEQUENCE
                                   NON_TER
                                                                                                                        STRAIN=IND.CAL1058;
                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                         Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003618; TFS2_cent
Pfam; PF00628; PHD; 1.
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InterPro; IPR001965; PHD.
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 198
198 /
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(TremBLrel. 17, Last sequence update)
(TremBLrel. 17, Last annotation update)
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Percent Identity:
                                                                  isolated from Calcutta, India.";
EMBL/GenBank/DDBJ databases.
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 51583AFE0BF1EDC1 CRC64;
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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123
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Copyright (c) 1993 - 2000 Comp
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1122.546 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

Query

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AW584724	AW584723	BE997991	AW586761	BE124753	AW616232	BG551208	AW432561	AW349333	BE659470	AW761136	ID
								w	_	AW761136 s	Description
N210839e	N210838e	EST42971	EST31838	EST39378	EST30727	sad34e05	sh75h06.	GM210007	GM7000091	s163f12.	
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Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

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BE519330	BE214475	BE346433	AW448025 ·	BG606610	AU084649	AI026312	AI443020	.BG605406	BF650924	AW459464	BG300821	AU101324	BF474495	BF275530	BE639441	AI726030	AI759012	BE123398	AI731699	BG320550	BG643885	BG605300	AI987319 ·	BE418763	BE039612	BE037301	BG048538	BG887479	BI208519	AW035325	8612	5511
BE519330 945023A05	BE214475 HV_CEb000	BE346433 sp25e05.y	AW448025 BRY_1261	BG606610 WHE2958_F	AU084649 AU084649	AI026312 L0-529T3	AI443020 sa30h05.y	BG605406 WHE2329_E	BF650924 NF098E01E	AW459464 sh41e10.y	BG300821 HVSMEb001	AU101324 AU101324	WHE0844_	BF275530 GAEb002	BE639441 946033B11	AI726030 BNLGH1139	AI759012 605085F11	BE123398 946001F06	AI731699 BNLGHi105	BG320550 Zm03_10h1	BG643885 EST512079	BG605300 WHE2331_B	AI987319 660003H05	BE418763 SCL074.H0	BE039612 OC01G11 O	BE037301 MP19C11 M	BG048538 OV1_14_H0	BG887479 EST513330	EST52	EST28	ΕS	sad33

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## ALIGNMENTS

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JOURNAL COMMENT REFERENCE AUTHORS VERSION KEYWORDS SOURCE RESULT AW761136 LOCUS ACCESSION DEFINITION TITLE ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. AW761136 530 bp mRNA EST 21-NOV-2000 s163f12.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-6024 5' similar to TR:065462 065462 RECEPTOR LIKE PROTEIN Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine Glycine AW761136 AW761136.1 GI:7693038 , mRNA sequence. (bases 1 to 530) Phaseoleae;

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Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Eabaceae; Papilionoideae; Phaseoleae
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               first-strand synthesis primer was used. An anchor nucleotide (V=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAACTAGTCTCGAG(T)18] to anchor the primer at the synthesis of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthexix Kit (catalog number 200401) was used to synthesize the cDNA. First-stranded synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XhoI; This cDNA library was constructed from mRNA isolated from cotyledons of 3- and 7-day-old Williams seedlings which were propagated on paper towels with distilled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="cotyledons of 3- and 7-day-old Williams
seedlings"
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/clone_lib="Gm-c1027"
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/db_xref="taxon:3847"
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98.6%;
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Pred. No. 3
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JOURNAL
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Best Local :
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                                                                                                                              482 CACTGACTGGT 472
                                                                                                                                                                                                                               542 GTATTGTAAATGTGAGATGCCTTNNAACCCTGATGACCTAATGGTGCAATGCGAGGGCTG 483
                                                                                                                                                        64 cactgactggt 74
                                                                                                                                                                                                                                                            4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctg 63
                                                                                                                                                                                                                                                                                                                                      68;
  AW349333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ystems.com web site:www.genomesystems.com
Seq primer: '5'.TTTTTTTTTTTTTTTTTT(A/C/G)-3'.
Location/Qualifiers
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Other_ESTs: AW432561 corresponding to Gm-c1015-5652 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program
Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edwin R. Madigan Building,
Tel: (217) 244-6147
Fax: (217) 333-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics
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                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-The library Gm-r1070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1070. The cDNA clones of the reracked Gm-r1070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/soybean/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l-vodkin@uiuc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The deta information on the source library for each clone can be obtained by referring to the Genome Systems clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.life.uiuc.edu/biotech/keck.html.corresponding 5' EST from each clone in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keck Center for Comparative and Functional Genomics, University of Illinois,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genomesystems.com, Keck Center for Comparative a
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95.8%;
764 bp
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Pred. No. 1
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                                                                                                                                                                                                                                              Local Similarity
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Tel: (217) 244-6147
Fax: (217) 333-4582
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Seq primer: 5'-TTTTTTTTTTTTTTTTT(A/C/G)-3'.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the laboratory of Linear Centers, University of Minnesota, Centers, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http:/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. The Gm-c1004 library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011 email: paul keim@nau.edu. virginia.coryell@nau.edu. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Computational Biology
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161 c 151 g 193 t 20 others
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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314 286 1810
                                                                                                                                                                                                                                                                                                                                     /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA fragments were directionally
                                                                                                                                                                                                                                                      cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was
                                                                                                                                                                                                 Erpelding."
                                                                                                                                                                                                                              constructed by Dr. Randy Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="GENOME SYSTEMS CLONE ID: Gm-c1015-5652"
/clone_lib="Gm-c1015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Mature flowers, field grown plants"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Glycine max"
                             52.5%;
94.4%;
Score 64.6; DB IV,
Pred. No. 1.2e-10;
""matches 4;
                                                                                                                                                                       138 g
                                                                                                                                                                                                                                    and Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schurk
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Query Match Best Local Matches

1 Similarity 67; Conserv

Conservative

Length 540;

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В Qy В QΥ

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONLact: SHOWNERS Project
Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          info@genomesystems.com web site: www.genomesystems.com High quality sequence stop: 380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 for further information call: (800) 430-0030 or (314) 427-322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max
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ID: Gm-c1074-2145 5' similar to TR:Q9SVI4 Q9SVI4 ES43 LIKE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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314 286 1810
(hypersensitive response) by vacuum infiltrating plant tissue with Pseudomonas syringae pv. glycinea carrying the avrB gene (Genetics 141:1597-1604). Plant tissue (expanded unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36, and 53 hrs after inoculation and their mRNA pooled equally for cDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from 9-11 day old seedlings that were induced for HR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1074-2145'
/clone_lib="Gm-c1074"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               response)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="seedlings induced for HR (hypersensitive
response"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="9-11 day old"
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4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctg

Query Match Best Local Matches

Similarity

49.98; 86.18;

Conservative

Pred. No. 1.3e 0; Mismatches Score 61.4; DB 10 Pred. No. 1.3e-09;

DB 10;

Length. 543; Indels

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ORIGIN
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AW616232
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                  van der Hoeven,R.S., Bezzeredes,J.L., Mattern,A.L., Holt,I.E., Liang,F., Hansen,T., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Mattin,G.B., Giovannoni,J.J. and Tanksley,S.D. Generation of ESTs from wild tomato (Lycopersicon hirsutum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryóta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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EST307271 L.
                                                                                                                                                                                                                                                                                                                             Clemson University
                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                 Contact: CUG
                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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AW616232
                                                                                                                                                                                                                                                                                       100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                likely with minor cells"
                                                   nitrogen, shearing off trichomes. This procedure yielded mixture of cells which is highly enriched for trichome likely with minor contaminations of other types of leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DHIOB host cells. Plant care, inoculations, and library construction were performed by Steve Clough (Lila Vodkin lab, University of Illinois).
                                                                                                      /clone_lib="L. hirsutum trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/note="Leaves of various stages were shaken in liquid
                                                                                                                                                                            /clone="cLHT1L23"
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                 /db_xref="taxon:62890"
                                                                                                                                                                                                                organism="Lycopersicon hirsutum"
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64 cactgactggt 74
                                                        4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctg
                                     GTATTGTAAATGTGAGATGCCCTACAACCCTGATGATCTGATGGTTCANTGTGAGGGCCTG 498
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BE124753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Agronomy and Plant Genetics University of Minnesota 411 Borlaug Hall, 1991 Upper Buford Circle, Tel: 612 625 5715 Fax: 651-649-5058 Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Carroll F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fedorova.M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,J.S., Pe,H., Ellis,L., Town,C.D., Bowman,C.D., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.

ESTs from one month old nitrogen-fixing root nodules of Medicago
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                                                                                                                                                                                                                               155
                                                                                                               Conservative
                                                                                                                                                                                                                   /dev_stage="effective root nodules harvested one month post inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhOI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meliloti. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."

55 a 114 c 137 g 167 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="pGVN-67F7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="GVN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'tissue_type="N2-fixing root nodules"
                                                                                                                               47.8%;
88.7%;
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                                                                                                             Score 58.8; DB 10
Pred. No. 8.9e-09;
0; Mismatches 8
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AW586761 514 bp mRNA EST 07-SEP-20 EST318384 MHAM Medicago truncatula/Glomus versiforme mixed library cDNA clone pMHAM-55G12, mRNA sequence. AW586761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mjharrison@noble.org
Noble EST name:N255126e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; mixed EST libraries 1 (bases 1 to 514)
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Tel: 580-223-5810
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seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                 Conservative
                                                                                                                                                                                                                                                                        /lab_host="E. coli strain XLOLR"
//note="Vector: pBluescript SK:, Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="roots colonized with Glomus versiforme" /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
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/clone="pMHAM-55G12"
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library"
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                                                                                                                                        47.38;
88.78;
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                                                                                                           Score 58.2; DB 10;
Pred. No. 1.4e-08;
0; Mismatches 8;
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Email: vance0046maroon.tc.umn.edu
University of Minnesota name: M271969e TIGR:
MTKAK29TK More information is available at:
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
AW584723 635 bp mRNA EST
N210838e MHAM Medicago truncatula/Glomus ven
Library cDNA clone MHAM-7K19, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="senescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old
plants harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage"
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/cultivar="genotype A17"
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed Eukaryota; mixed EST libraries.
                                                                                                                                             AW584724 655 bp mRNA I
N210839e MHAM Medicago truncatula/Glomus
                                                                                   AW584724.1
                                                                                                      AW584724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mjharrison@noble.org
Other name: MHAM-7a-F10; Date: 3/14/00; Updated to the Database of
Expressed Sequence Tags (dbEST) on 04/27/00; More information is
available at http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.. Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C., Elms from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed Eukaryota; mixed EST libraries.
                                                                                                                          library cDNA clone MHAM-7K21, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Harrison M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
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580-221-7380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 day
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_bost="E. colistrain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2 XhoI; CDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from
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/db_xref="taxon:119092"
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                                                                                   GI:7261778
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Medicago truncatula/Glomus versiforme mixed EST library.

Medicago truncatula/Glomus versiforme mixed EST library

Medicago truncatula/Glomus versiforme mixed EST library

Eukaryota; mixed EST libraries.

1 (bases 1 to 682)

1 (bases 1 to 682)

1 (bases 1 to 682)

Harrison, M.J., Liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C.D.,

Rowman.C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library cDNA clone MHAM-7J12, mRNA
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Other name: MHAM-7a-Fl1; Date: 3/14/00; Updated to the Database
Expressed Sequence Tags (dbEST) on 04/27/00; More information is
available at 'http://chrysie.tamu.edu/medicago'.
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/clone="MHAM-7K21"
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               Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna, A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                        Glycine max
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Other name: MHAM-7d-E06; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580-223-5810
Fax: 580-221-7380
                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Public Soybean EST Project
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/db_xref="taxon:119092"
/clone="MHAM-7J12"
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Pred. No. 1.4e-08;
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EST244450 tomato ovary,
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                         AI486129.1
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                                                                                                               cLED5K16, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                              tomato.
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High quality sequence stop: 421.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for CDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DHIOB host cells. Plant care, inoculations, and library construction were performed by Steve Clough (Lila Vodkin lab, University of Illinois)."
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/lab_host="DH10B"
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/clone_lib="Gm-c1074"
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/db_xref="taxon:3847"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                       Clemson University
100 Jordan Hall, C
                                                                                                                                     , Liang, F., Upton, J., Craven, M.B., Bowman, C.L., ,C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. & Generation of ESTs from tomato callus tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW035325 608 bp mRNA EST 18-MAY-2001 EST280688 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC40J12 similar to A. thaliana ES43-like protein, mRNA sequence
                                                                  Clemson University Genomics Institute
                                                                                            Contact: CUGI
                                                                                                             Unpublished (1999)
                                                                                                                                                                                                          Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T.,
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Email: http://www.genome.clemson.edu/orders/index.html
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Clemson,

SC 29634, USA

and Giovannoni, J Ahn,S., Ronning

Holt, I.E.

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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,C.L., Nierman,W., Fras, S.D. and Giovannoni,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                Conservative
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                                                                                                                                                                                                                                                         respectively.
                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4081"
/clone="cleD5K16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="tomato ovary, TAMU"
                                                                                                                 46.0%;
87.3%;
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                                                                                              0;
                                                                                              Score 56.6; DB 10;
Pred. No. 4.1e-08;
0; Mismatches 9;
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                                                                                                                                            Length 335;
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XhoI sitee
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Solanum;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Generation of ESTs from Tomato Suspension
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI208519.1 GI:14686243
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l: http://www.genome.clemson.edu/orders/index.html.
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/note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Suspension cultures of L.esculentum E5203 were grown in Murashige and Skoog based medium, supplemented with 15% coconut milk (filter sterilized and added after autoclaving), 2% saccharose, and lmg/ml 2,4D (pH5.8). Fresh medium was added every 7 days, and cultures were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; supplier: Giovannoni laboratory; cLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library" 149 c 147 g 154 t
                                                                                                                                                                    /cultivar="TA496, E6203"
/db_xref="taxon:4081"
/clone="cTOS1768"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 538
                                                                                                               /tissue_type="suspension cultures"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF'"
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/clone_lib="tomato callus, TAMU"
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/db_xref="taxon:4081"
                                                                                                                                                     /clone_lib="cTOS"
                                                                                                                                                                                                                        organism="Lycopersicon esculentum"
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cTOS17G8 5'
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Query Match
Best Local Similarity
511 GTACTGTAAATGTGAAATGCCATACAATCCTGATGACCTCATGGTTCAATGTGAGGGCTG
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                     4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgaagggctg
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1 (bases 1 to 732)
van der Hoeven, R., Bezzerides, J., Ewing, E., Cho, J., Chiemingo, A.,
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EST513330 CSTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generations of ESTs from dormant potato tubers Unpublished (2001)
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                                                                                                                                                                                                   /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were store for one month post-harvest at 4oC. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    grown at shaking."
                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="dormant tuber"
/dev_stage="one month post-harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="cSTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="cSTD5N3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism≈"Solanum tuberosum"
/cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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87.3%;
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                                                                               Score 56.6; DB 11;
Pred. No. 4.8e-08;
0; Mismatches 9;
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Pred. No. 4.7e-08;
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                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ewing, E., Cho, J., Chiemin Tanksley, S. and Baker, B.
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cSTD5N3 5' sequent
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RESULT 1
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                                                                                                                                                                                                                                   64 cactgactggtaagtttcacatgtaaggtg 93
                                                                                                                                                                                                                                                                                       4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctg 63
                                                                                                                                                                                                      CAAGGACTGGTTCCATCCATCTTGCATGTG 141
                                                                                                                                                                                                                                                                      GTATTGCAAATGTGAGATGCCATACAACCCTGATGACCTCATGGTGCAGTGCGACGCTTG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
BG048538
                                                                                             BE037301 674 bp mRNA I
MP19C11 MP Mesembryanthemum crystallinum
                                                                                                                                                                                                                                                                                                                                     69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502,
Mesembryanthemum crystallinum
                                                                    BE03730
                 common ice
                                                   BE037301.1
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1 (bases 1 to 541)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG048538.1
EST.
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OV1_14_H02.g2_A002
                                                                                  like protein, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An EST database from Sorghum: Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Ovary 1 (OV1)"
/note="Organ: Mix of ovaries of varying immature stages
/note="Organ: Mix of ovaries of varying immature stages
/note="Organ: Mix of ovaries of varying immature stages
/note="Organ: Stage: Vector: paluescript II from Lambda
Zap II, Site_1: XhoI; Site_2: EccRI; The library was made
from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."

111 c 141 g 150 t
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/db_xref="taxon:4558"
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                 plant
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2 Ovary
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Pred. No. 5.3e-08;
Pred. No. 5.3e-21;
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AUTHORS
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                                                                                                                                                                                                                                              1 (bases 1 to 959)
Bohnert, H. J., Borchert, C., Brazille, S., Brooks, J.,
H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE039612 959 bp
OC01G11 OC Oryza sativa
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., H., Kawasaki, S., McCollough, A., Mchalowski, C.B., Scara, G., Wheeler, M. and Zepeda, G.R. Functional Genomics of Plant Stress Tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.

1 (bases 1 to 674)
                                                                                                                                               Fax: 520-621-1697
                                                                                                                                                                Tel: 520-621-7982
                                                                                                                                                                                  Bio Sciences West room 513,
                                                                                                                                                                                                 University of Arizona
                                                                                                                                                                                                                    Contact: Michalowski, C.B.
                                                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE039612.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE03961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cbm@u.arizona.edu.
Location/Qualifiers
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                                                                                                          cbm@u.arizona.edu
Length: 1 Std E
/db_xref="taxon:4530"
/clone_lib="OC"
                                 /organism="Oryza sativa"
/strain="Pokkali"
                                                                                   ngth: 1 Std Error:
Location/Qualifiers
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/dev_stage="6 weeks"
/note="3 d 500mm Nacl"
184 c 164 g 155 t
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/db_xref="taxon:3544"
/clone_lib="MP"
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NO. 1.8e-07;
smatches 12;
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Palacio,C.,
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Palacio,C
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                            GTACTGCAAGTGCGAGATGCCGTATAACCCGGATGATCTAATGGTGCAGTGCGAGGGATG 138
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cactgactggtaagtttca
                                                                                                                                                                                                                                                                                                                                                                       Email: scloutier@em.agr.ca
International Triticeae EST Coop
http://wheat.pw.usda.gov/genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Laro, G.R., Lin, J.J., McGuire, P., Oglhara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.
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Triticum aestivum
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SCL074.H01R990724 ITEC
CDNA clone SCL074.H01,
                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 204 983 2340 Fax: 204 983 4604
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Winnipeg MT CANADA
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                                                                                                                                                                                           /clone_lib="ITEC SCL Wheat Leaf Library"
/tissue_type="young leaf"
/dev_stage="after 24 hour challenge with LR-AVR1"
/note="Vector: Lambda ZAP; 1.0 Kbp average insert size."
1 231 c 248 g 175 t 42 others
                                                                                                                                                                                                                                                                             /db_xref="taxon:4565"
/clone="scro74 ....
                                                                                                                                                                                                                                                                                                        /organism="Triticum aestivum"
/cultivar="Thatcher_Lr1"
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                                                                                                                   BG605300 675 bp mRNA EST 16-APR-2001 WHE2331_B03_D05ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE2331_B03_D05, mRNA sequence.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Triticem.
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                                         Triticum aestivum
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                                                                                         BG605300.1
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Plate: 660003 row: H column:
Location/Qualifiers
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855 California Ave, Palo
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Contact: Walbot V
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a 129 c 113 g 135 t
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/clone_lib="660 - Mixed stages of anther and pollen"
/tissue_type="whole premieotic anthers to pollen shed"
/dev_stage="premieotic anthers to pollen shed"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
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BG643885.1
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            van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
                                                                                                                          Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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US Department of Agriculture, Agriculture Research Service,
West Area, Western Regional Research Center
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The structure and function of the exp
Unpublished (2001)
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                                                                                                              Asteridae;
                                                                                                                                                                                           tomato.
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derson,O.D., Chao,S., Choi,D.W., Close,T.J., Fo
                                                                        (bases 1 to 726)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4765"
/clone="WHE2331_B03_D05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                            euasterids I; Solanales;
                                                                                                                                                                                                                               GI:13779110
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79.78;
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Pred.
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No. 5.1e-07;
                                                                                                          Solanaceae;
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                                                                                                              Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rausch, C.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60;
                                                                                                                                                                                                          Agriculture and Agri-food
960 Carling Avenue, Bldg.
Tel: (613) 759-1662
Fax: (613) 759-1701
                                                                                                                                                                                                                                                                                    Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zm03_10h12_A zm03_AAFC_
cDNA clone zm03_10h12,
                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                               Under High Light Intensity
                                                                                                                                                                                                                                                                                                                                                                 Expressed Sequence Tags from Cold-Stressed Maize Seedlings Grown
                                                                                                                                                                                                                                                                                                                                                                                       and Tinker, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Simmonds, J.A., Singh, J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG320550.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: http://www.genome.clemson.edu/orders/index.html
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: CUGI
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 449)
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                                                                                                                                                                                                                                                                                                                                                                                                     Harris,L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                  singhja@em.agr.ca.
Location/Qualifiers
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148 c 148 g 201 t
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                  /tissue_type="Leaf, crown"
/dev_stage="4-leaf"
                                                                                                              /organism="Zea mays"
/cultivar="CO328"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2:
/note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2:
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: Eco RI;
                                                    /clone_lib="Zm03_AAFC_ECORC_cold_stressed_maize_seedlings"
                                                                          /db_xref="taxon:4577"
/clone="Zm03_10h12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="cTOF33K11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lycopersicon
/cultivar="TA496"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.48;
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AAFC_ECORC_cold_stressed_maize_seedlings Zea mays
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Pred. No. 5.2e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence
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J.I., Ouellet,T., R
                                                                                                                                                                                                                                                  Ottawa, Ontario,
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Sprott,D.
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                           64. cactgactggta 75
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                                                        tgcactgactggtaagtttca 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     upland cotton.
Gossypium hirsutum
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                       60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI731699 672 bp mRNA EST 11-JUN-1999 BNLGHill0507 Six-day Cotton fiber Gossypium hirsutum cDNA 5's to (AL022140) receptor like protein (fragment) [Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                    Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3307
Fax: 516-344-3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biology Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Ben Burr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESTs from developing cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.
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AI731699
                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: T3 Primer
                                                                                                                                                                                                                                                                                                                                                                                                     Email: burr@bnlux1.bnl.gov
                                                                                                                                      Similarity
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                                                                                                                                                                                                                                            /clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XL1-Blue"
                                                                                                                                                                                                                  /note="Vector: pBluescript II KS+" 131 c 159 g 192 t
                                                                                                                                                                                                                                                                                                           /cultivar="Acala Maxxa"
/db_xref="taxon:3635"
                                                                                                                                                                                                                                                                                                                                         /organism="Gossypium hirsutum"
                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             . 672
                                                                                                                                      42.9%;
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77.8%;
                                                                                                                      Score 52.8; DB 10;
Pred. No. 8e-07;
0; Mismatches 12;
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RESULT 28
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                    EST
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BE123398
BE123398.1 GI:8516673
                                          Zea mays
                                                     Zea mays.
                                                                                                          CDNA, mRNA
                                                                                                                                      AI759012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: walbot@stanford.edu
Plate: 946001 row: F colu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         855 California Ave,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Biological Stanford University
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library in Hybr12AP. Sample insert size
to 3 Kb with a 1 Kb average."
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/dev_stage="just after the
inflorescence development"
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/cultivar="0H43"
/db_xref="taxon:4577"
/clone_lib="946 - tassel primordium
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Pred. No. 1.3e-06;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AI726030 672 bp mRNA EST 11-JUN-1999 BNLGH113981 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AL022140) receptor like protein (fragment) [Arabidopsis
                                                                                                                    Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
                                                                                                                                                                         Contact: Ben Burr
Biology Department
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Contact: Walbot V
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                                                                                                                                                                                                                                                                                                                                                                           EST
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AI726030.1
                                                                 Fax: 516-344-3407
Email: burr@bnlux1.bnl.gov
Seq primer: T3 Primer.
                                                                                                                                                                                                                            ESTs from developing cotton fiber
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Tel: 650 723 2227
Fax: 650 725 8221
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Maize ESTs from various cDNA libraries sequenced
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Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
/organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
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/cultivar="Ohlo43"
/cultivar="Ohlo43"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
/lab_host="DH5(alpha)"
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                                                                                                                                                                                                                                                                                                                               Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946033 row: B column: 11.
Location/Qualifiers
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855 California Ave, Palo Alto,
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Contact: Walbot V
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/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tasse
                                                                                     Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the library in HybriZAP. Sample insert size range was 30 to 3 Kb with a 1 Kb average."
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/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="%XL1-Blue"
/note="Vector: pBluescript II KS+"
162 c 145 g 190 t 1
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BF474495
BF474495.1 GI:11543677
                                                                                                                                                                                                                                                          66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wing.R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A. An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 864 656 7288
Fax: 864 656 4293
Email: rving@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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213 c 214 g 211 t 1 others
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/clone="GA_Eb0024E174"
/clone_ib="GOssyptum arboreum 7-10 dpa fiber library"
/cissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gossypium arboreum"
/strain="AKA"
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KEYWORDS
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                    Oryza sativa Oryza sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaae; Oryza.
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
RANN Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The structure and Tong, J.C.

The structure are a few structure are all the structure are a few structures 
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Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/tissue_type="Crown tissue of seedling"
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Contact: Takuji Sasaki
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
National Institute of Agrobiological Resources
                                                                                                                                                                                                                                               1 (bases 1 to 861)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
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305-8602,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
                                                                                             Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                           Clemson University
100 Jordan Hall, Clemson,
                                                             Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                          Clemson University Genomics Institute
                                                                                                                                                                             Contact: Wing RA
                                                                                                                                                                                          for barley genomics
Unpublished (2000)
                                                                                                                                                                                                                        Development of a genetically and physically anchored
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                           Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                          barley.
                                                                                                                                                                                                                                                                                                                                                                                                                        BG300821.1 GI:13098348
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Fax: 81-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E10910_8Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki,T. and Yamamoto,K.
Rice cDNA from panicle at ripening stage (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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a 149 c
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/strain="Nipponbare"
/db_xref="taxon:4530"
/clone="E10910"
                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Rice panicle at ripening stage"
/dev_stage="ripening stage"
/note="Organ: panicle; Rice cDNA from panicle at ripening
/organism="Hordeum vulgare"
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81.7%;
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ies 13;
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Best Local (
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339 CAAAGACTGGTTCCATCCA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna, A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW459464 420 bp mRNA EST 17-JUL-2000 sh41e10.yl Gm-c1017 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1017-4291 5' similar to TR:065462 065462 RECEPTOR LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                            This clone is available through: Genome Systems, Inc. 4633 Mc Parkway Circle St. Louis, Missouri 63134 For further informat call: (800) 430-0030 or (314) 427-3222 FAX:(880) 919-3324 or 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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                                                                                                                                                                            High quality sequence stop:
                                                                                                                                                                                                                                  Insert Length: 451
                                                                                                                                                                                                                                                                    info@genomesystems.com web site: www.genomesystems.com
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more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
a 209 c 230 g 197 t 3 others
/clone="GENOME SYSTEMS CLONE ID: Gm-c1017-4291"
/clone_11b="Gm-c1017"
                                                         /organism="Glycine max"
/db_xref="taxon:3847"
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/db_xref="taxon:4513"
/clone="HysMEb0018I16f"
/clone_lib="Hordeum vulgare seedling shoot EST library
/HVcDNA0002 (Dehydration stress)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            St. Louis, MO 63108,
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                                                                                                                                                                                                                                                                                                                                                        Systems, Inc. 4633 World For further information
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RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF650924 539 bp mRNA EST 20-DEC-2000 NF09BE01EC1F1005 Elicited cell culture Medicago truncatula cDNA clone NF09BE01EC 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact. Contact Plant Biology Division
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Of 73402, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Center for Medicago Genomics Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Trifolieae; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST.
                                                                                                                                                                                                                                                                                  Email: radixon@noble.org
Insert Length: 539 STA Error: 0.00
Platte: 098 row: E column: 01
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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              /clone_lib="Elicited cell culture"
/clone_lib="Elicited cell culture"
/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
/dev_stage="Cell suspensions days after subculture"
days. Cells were induced six days after subculture"
                                                                                                                                          /db_xref="taxon:3880"
/clone="NF098E01EC"
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74 c
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/lab_host="XL10-Gold"
/note="vector: pBluescript II XR; Site_1: EcoRI; Site_2:
/note="Vector: Lambda Zap; Cells were induced with yeast
                                                                                                                                                                                                  /organism="Medicago truncatula"
                                                                                                                                                                                                                                                     ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service,
West Area, Western Regional Research Center
And Bunchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG605406 586 bp mRNA EST 16-APR-2001 WHE2329_E06_I11zS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE2329_E06_I11, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence with phred score less Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 586)
Anderson,O.D., Chao,S., Choi,D.W., Clc,P.S., Hsia.C.C., Kang,Y., Lazo,G.R., Seaton,C.L. and Tong,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
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                    poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                  /Clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coll SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation." a 108 c 125 g 157 t 3 others
                                                                                                                                                                                       greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Triticum aestivum"
/cultivar="Chinese Spring"
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Pred. No. 9.7e-06;
Pred. No. 9.7e-06;
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a; Poales; Poaceae; Pooidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khann, A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C Wylie,T., Underwood,K., Steptoe,M., Thising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuri,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                                                                This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 Foor further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com Insert Length: 1604 Std Error: 0.00 Seq.primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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sa30h05.yl Gm-c1004 Glyc
Gm-c1004-850 5' similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
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/note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; Root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA
                                                                                                                                                                                                                                                                  /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID:
                                                                                                                                                                                                         /tissue_type="root"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                 /clone_lib="Gm-c1004"
                                                                                                                                                                                                                                                                                                      organism="Glycine max"
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                                                                                                                                                                                          Plate: L0-6
                                                                                                                                                                                                                   BACKWARD:
                                                                                                                                                                                                                                                                                                                                                   MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biochemistry
University of Nevada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Cushman JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
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                                                                                                                                                                                                                                                                                                   Email: jcushman@unr.edu
                                                                                                                                                                                                                                                                                                                               Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An expressed sequence tag database for the common ice plant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                              primer: T3
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                                                                                                        quality sequence stop: 340.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmids with cDNA inserts. Blue colonies 9n-15) have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, Az 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, email: paul.keim@nau.edu, virginia.coryell@nau.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the CDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' CDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that had been digested with ECORI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant the white and blue colonies appear to contain recombinant
                         /organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
                                                                                    1. .380
/clone="L0-529"
                                                                                                                                                                                                                   Τ3
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79.5%;
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Pred. No.
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ches 15;
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/clone\_lib="Ice plant Lambda Uni-Zap XR expression library

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ORIGIN
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                                                                                                         Query Match
Best Local Similarity
Matches 57; Conserv
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                                                 Local
              cactgactggt 74
TAAAGACTGGT 488
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AU084649.1
EST.
                                                                                                                                                                                                                                                                                                                                             Cryptomeria japonica
Plant Mol. Biol. 43, 451-457 (2000)
Contact: Tokuko Ujino-Ihara
Bio-resources Technology Division
Porestry and Forest Products Research Institute
Matsunosato 1, Kukizaki, Ibaraki 305-8687, Japan
Tel: 81-298-73-3211(ex.444)
Fax: 81-298-73-3795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cryptomeria japonica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU084649 490 bp mRNA E AU084649 Cryptomeria japonica inner bark clone CC1649 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                      Email: udino@ffpri.affrc.go.jp;
URL:http://www.ffpri.affrc.go.jp/labs/cjgenome/database/cjdatae.htm
1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 57; Conserver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ujino-Ihara,T., Yoshimura,K., Ugawa,Y., Yoshimaru,H., Nagasaka,K. and Tsumura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expression analysis of ESTs derived from the inner bark of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cryptomeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Japanese cedar.
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                                                                                                           Conservative
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                                                                                                                                                                                      /organism="Cryptomeria japonica"
/db_xref="taxon:3369"
/clone="CC1649"
/clone_lib="Cryptomeria japonica inner
/cissue_type="inner bark"
1 99 c 141 g 115 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
ECORI; Site_2: XhoI"
69 c 96 g 113 t
                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/dev_stage="Six week old"
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80.3%;
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                                                                                                        Score 48.6; DB 10;
Pred. No. 1.7e-05;
0; Mismatches 14;
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Pred. No. 1
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nes 14;
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Cryptomeria
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RESULT 42
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                                                                                                                                               412 CTCTGATTGGT
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                                                                                                                                                                     64 cactgactggt 74
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AW448025 658 bp mRNA EST 03-JAN-2001
BRY_1261 BRY Triticum aestivum cDNA clone P28-2A, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                    l Similarity
57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l (bases 1 to 558)
Anderson,O.D., Chao,S., Chin,A., Close,T.J., Doherty,L., Fenton,R.D., Lazo,G.R., Rausch,C.J., Walker-Simmons,M.K. and Wilson,C. The structure and function of the expressed portion of the wheat genomes - Dormant embryo cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
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BG606610
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Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Olin Anderson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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Tel: 5105595773
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/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown to seed
maturity under conditions favoring seed dormancy (L.
Dohery at K. Walker_Simmons lab, Washington State
University, Pullman, WA). Embryos were cut from mature
dormant seed (Doherty). Total RNA was prepared from these
embryos, polyA was purified, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
phagemids in the TJ Close lab at the University of
California, Riverside (Chin, Fenton). Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

62 a 115 c 149 g 131 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Seed embryo"
/dev_stage="Mature seed"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="WHE2958_F12_L24"
/clone_lib="Wheat dormant
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les 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 cactgactggt 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgaagggctg 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTGATTGGT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTTTGTAAGTGTGAGATGCCATACAACCCTGATGATCTTATGATCCAGTGTGAGGAATG 582
                                                                                       Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                       BE346433 594 bp mRNA EST 18-JUL-2000 sp25e05.yl Gm-c1042 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1042-1593 5' similar to TR:065462 065462 RECEPTOR LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPO Box 1600, Canberra, ACT, Australia
Tel: 61 2 6246 5054
Fax: 61 2 6246 5000
Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                     Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project
                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                          Glycine max
                                                                                                                                                                                                                                                                                                                                                                BE346433
BE346433.1 GI:9258286
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Bryan Clarke
Division of Plant Industry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clarke, B.C., Hobbs, M. and Appels, R. Genes active in developing wheat endosperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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                                                                           Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: bryanc@pi.csiro.au.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bread wheat
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                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
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186 c 176 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4565"
/clone="P28-2A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="BRY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar="Wyuna"
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 St. Louis, MO 63108, USA
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BASE COUNT
ORIGIN
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SOURCE
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BE214475/c
                                                                COMMENT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgaagggctg 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGGATTGGTA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cactgactggta 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE214475 706 bp mRNA EST 09-MAR-2001 HV_CEb0003J01f Hordeum vulgare seedling green leaf EST library HV_CDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA (HV_CEb0003J01f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
                                                                                                                                                                            1 (bases 1 to 706)
Wing,R, Close,T.J., Kleinhofs,A., Wise,R., Be
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,
,T., Saski,C., Schwartzbeck,J., Simmons,J., Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                         HVcDNA0005 (Erysiphe
HV_CEb0003J01f, mRNA
BE214475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
Call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                        Contact: Wing RA Clemson University Genomics Institute
                                                                                    Development of a genetically for barley genomics Unpublished (2000)
                Clemson University
                                                                                                                                                            Wood, T.
                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            info@genomesystems.com web site: www.genomesystems.com
100 Jordan Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 79.: 57; Conservative
                                                                                                                                                                                                                                                                            Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               were grown in a growth chamber using germination paper. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gloco BRJ). This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from 2 week old seedlings with the cotyledons removed at the time of harvest. The seedlings for the cultivar Raiden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XhoI; This cDNA library was constructed from mRNA isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library was constructed by Dr. Randy Shoemaker."
112 c 168 g 156 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Whole seedling without cotyledons"
/lab_host="DH10B"
/note="Vector: pBluescriptII SK+; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="GENOME SYSTEMS CLONE ID: Gm-c1042-1593"
/clone_lib="Gm-c1042"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Glycine max"
/db_xref="taxon:3847"
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79.2%;
Clemson,
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Pred. No. 2
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SC
29634, USA
                                                                                                                                 and physically anchored
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2.8e-05;
15;
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                                                                                                                                                                                                    Begum, D., Frisch, D., Yi
le, S., Palmer, M., Rambo
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ACCESSION
VERSION
KEYWORDS
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BE519330
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Best Local 9
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                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE519330 444 bp mRNA
945023A05.yl 945 - Mixed adult tissues
(SK) Zea mays CDNA, mRNA sequence.
BE519330
BE519330.1 GI:9743182
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Email: rwing@clemson.edu
Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 4
High quality sequence stop: 630.
                                                                                                                                                                                                                             Email: walbot@stanford.edu
Plate: 945023 row: A colu
                                                                                                                                                                                                                                                                                                                                                                                                                                   Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                             University
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                                                                           /db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues
same as 707 (SK)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 182 c 147 g 187 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hordeum vulgare"
/cultivar="CI16151 (Mla6)"
/db_xref="faxon:4513"
/clone="HV_CEb0003J01f"
/clone="HV_CEb0003J01f"
vlone=lib="Hordeum vulgare seedling green leaf EST library HVcDNA0005 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/tissue_type="seedling green leaf"
/note="Organ: tassel, kernal, silk, husk, root, leaf;
                   /tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
                                                                                                                                           /organism="Zea mays"
/cultivar="W23"
                                                                                                                                                                                                     Location/Qualifiers
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Pred. No. 2.9e-05;
0; Mismatches 20;
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> 124 a Vector: pGAD10; Site\_1: ECORI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing." a 95 c 109 g 116 t

Matches Query Match Best Local : Local Similarity 56; Conservative 38.2%; 0; Score 47; DB 10; Pred. No. 5.6e-05; Mismatches 15; Length 444; Indels Gaps

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ORIGIN BASE COUNT

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Q 64 cactgactggt 74

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297 TTCTGACTGGT 307

Search completed: March 19, 2002, 10:18:40 Job time: 2754 sec

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180 601 66 288

pathway;
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Sequence

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XX Arabidopsis thaliana.

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99US-0155486 99US-0155659

99US-0156458

990S-0157117 990S-0157753

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seq_documentation_block:
ID AAB93780 standard; Protein; 790 AA
XX
AC AAB93780;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:1
XX
KW Human; primer; detection; diagnosi
XX
OS Homo sapiens.
XX
EP1074617-A2.
                                                                                                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB93780
                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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                                                                                                                                                                                                                                                                                                            Percent Similarity:
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21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
                                                            Human protein sequence SEQ ID NO:13511.
                                                                                                                                                                            296
                                                                                                                                                                                                                                                                                                                                                             28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                   280 PheCysLysCysGluMetProTyrAsnProAspAspLeuMetValGlnCy 296
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                                                                                                                                                                                             55 CGAGGGCTGCACTGACTGG
                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                           TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG 54
                                                                                                                                                                          sGluGluCysSerGluTrp
                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                       Ratio:
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99US-0161993.
99US-0162142.
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99US-0161359.
99US-0161360.
99US-0161361.
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99US-0161404.
99US-0161405.
                                        detection; diagnosis; antisense therapy; gene therapy.
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990S-0160815.
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99US-0160770.
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5.636
95.652
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                                                                                                                                                                                                                                                                                                            Percent Identity: 78.
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0
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The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of CC cligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 5'-end CC oligonucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a composition of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primers sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB45893 represent human amino acid sequences; and AAH13629 to AAH13620 crepresent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 13511; 2537pp + CD ROM; English
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Sugiyama T, Wakama
    790
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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    AA;
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Wakamatsu
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A, Nagai K,
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Otsuki
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alignment_block:
US-09-684-016-48411 x AAB93780
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                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                     Align seg 1/1 to: AAB93780
                        55
 23
             CGAGGGCTGCACTGACTGG 73
                                                 TyrCysLeuCysArgLeuProTyrAspValThrArgPheMetIleGluCy 23
                                                                            TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG 54
sAspMetCysGlnAspTrp
                                                                                                                                                                                               Quality:
                                                                                                                                                                    74.00
4.625
69.565
 29
                                                                                                      from: 1
                                                                                                                                                                 Gaps:
Percent Identity:
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0:
                                                                                                      790
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0
43.478
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seq\_documentation\_block:
ID AAB42371 standard; Protein; 1084 AA.

seq\_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAB42371

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antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1999;
02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                        antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                 AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary, antiposciatic appropriations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellins; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                  erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC74446 to AAC77606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimkets
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vulnerary; antipsoriatic; antiparkinsonian;
anticonvulsant; osteopathic; antiarthritic;
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DB; AAC76580.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 3476-3478; 5507pp; English.
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99US-0127636.
99US-0127728.
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                                  as a contraceptive
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immunosuppressant;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    documentation_block:
      The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAW42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide in gene therapy be used to treat diseases of the peripheral nervous of the invention may be used to treat diseases of the peripheral nervous
                                                                                                  Novel nucleic acids and such as central nervous
                                                                                                                                                                              Wang
                                                                                                                                                                                        Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                     peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; Haemostatic; amyotrophic lateral sclerosis; BNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                   N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia.
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TY
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DB; AAI60138.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nootropic;
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                                                                            2;
                                                                                                                                                                  Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                              HYSEQ INC
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2000US-0552317.

2000US-05598042.

2000US-0620312.

2000US-0621450.

2000US-0662191.

2000US-0693036.

2000US-0727344.
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4.625
69.565
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressant; cytostatic;
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                                                                                                                                                                  Goodrich
                                                                             5913;
                                                                                                  polypeptides,
system injuri
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 nervous
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Xu C,
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                                                                                                  injuries
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injuries, peripheral
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Xue
                                                                                                           useful
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RT;
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0
43.478
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Yang Y,
                                                                                                            for
                                                                                                             treating
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Zhang
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                                                                                                              disorders
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                                                                                                                                                                                        Wang
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seq_documentation_block:
ID AAM39196 standard; P.
XX
AC AAM39196;
XX
DT 22-OCT-2001 (first of the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance. peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TyrCysIleCysLysArgProTyr...ProAspProGluAspGluIlePr 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM39196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 425 AA
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2000US-0598042
2000US-0620312
2000US-0653450
2000US-0662191
2000US-0693036
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4.433
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Wehrman T,
Goodrich R
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Xu C,
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Drmanac R
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Gaps: 2
Identity: 48.276
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Xue AJ,
ac RT;
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                                                                                           Ren F,
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seq_documentation_block:
ID AAB60498 standard; PA
XX
AC AAB60498;
XX
24-APR-2001 (first 6
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DT 24-APR-2001 cycle and
DE Human cell cycle and
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Cell cycle and prolli
KW Cell cycle and prolli
KW antagonist; gene thei
KW transgenic animal disord
KW developmental disord
KW cell proliferative di
KW arteriosclerosis; asi
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OS Homo sapiens.
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PN W0200107471-A2.
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PD 01-FEB-2001.
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PPF 21-JUL-2000; 2000WO-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypuncleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                            transgenic animal disease model; immune disorder; developmental disorder; cell signalling disorder; cell proliferative disorder; cancer; tumour; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                        menstrual cycle disorder; bacterial infection.
                                                                                                                                                                                                                                                                                        Cell cycle and proliferation protein; CCYPR; human; antagonist; gene therapy; detection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                        Human cell cycle and proliferation protein CCYPR-46,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB60498 standard; Protein; 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO 2341; 10078pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt oAspGluMetIleGlnCysValValCysGluAspTrp}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTGTAAATGTGAGATGCCTTACAACCCTGAT......
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The sequer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for receptor activity, arthritis and inflammation,
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                         2000WO-US19948
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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4.433
51.724
                                                                                                                                                                                                               asthma; allergy;
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                                                                                                                                                                                                             diabetes mellitus;
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48.276
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                                                                                                                                                                                                                                epilepsy;
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promoter;

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seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             to CCYPR may be used in enzyme-linked immunosorbent assays (ELISA) or radioimmunosasys to detect CCYPR. CCYPR itself may be used to detect Ccompounds e.g., antibodies, oligonucleotides and proteins (receptors) that specifically bind to CCYPR, and in drug screening methods to Ccypr identify compounds that modulate the activity of CCYPR. CCYPR concleotides can be used to generate transgenic animal models of human concleotides and can be used in gene therapy in target cells with genetic abnormalities with respect to the expression of CCYPR for the treatment or prevention of a disorder associated with CCYPR. CCYPR concleotions, nucleic acids, agonists or antagonists include immune, conclude immune, conclude including cancer. Specific examples of these disorders including cancer. Specific examples of these disorders, allergies, attention of the proteins, and cell signalling disorders.
                                                                                                                                                                                                                                                          Align seg 1/1 to:
                                                                                                                                                                                                                                                                                   US-09-684-016-48411 x AAB60498
                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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08-SEP-1999;
10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAB60453-AAB60506 represent 54 human cell cycle and proliferation proteins (CCYPR), which are encoded by AAF59590-AAF59643. CCYPR and agonists of CCYPR are used to treat diseases or conditions associated with decreased expression of functional CCYPR, while CCYPR antagonists are used to treat diseases or conditions associated with overexpression of functional CCYPR. Monoclonal or polyclonal antibodies
              Arabidopsis thaliana protein fragment SEQ ID
                                                                                                                                                         149
                                                                                                                                                                                                      134 TyrCysIleCysLysArgProTyr...ProAspProGluAspGluIlePr 149
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
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N-PSDB; AAF59635.
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                                                                                                                                                       oAspGluMetIleGlnCysValValCysGluAspTrp 161
                                                                                                                                                                                                                                TATTGTAAATGTGAGATGCCTTACAACCCTGAT.........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n cell cycle and proliferation proteins and polynucleotides are
to treat, diagnose and prevent immune, developmental and cell
aling disorders and cell proliferative disorders including cancer
                                                                                                                                                                                .GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGG
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                                                                                         standard; Protein; 193
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                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                           bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                  425
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Yang
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99US-0153129.
99US-0164647.
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Lu DAM,
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Baughn MR,
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Gaps:
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R, Patterson
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C, Shah P;
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  18-JUN-1999
18-JUN-1999
18-JUN-1999
18-JUN-1999
18-JUN-1999
18-JUN-1999
22-JUN-1999
23-JUN-1999
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17-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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19-MAY:1999
20-MAY:1999
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27-MAY:1999
27-MAY:1999
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23-APR-1999
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04-MAY-1999
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16-APR-1999;
19-APR-1999;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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14-MAY-1999;
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06-APR-1999;
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Gaps:
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                                                                                                                                                                                  Align seg 1/1
                                                                                                                                                                                                                    US-09-684-016-48411 x AAY04323
                                                                                                                                                                                                                                                                        Percent Similarity:
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29-AUG-1997;
29-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
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                                   sAspArgCysGlnAsnTrp 83
                                                                       CGAGGGCTGCACTGACTGG 73
                                                                                                         TyrCysIleCysArgThrProTyrAspGluSerGlnPheTyrIleGlyCy
                                                                                                                                              TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
/SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAY57453
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seq_documentation_block:
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                                                                                                                                                      2620
                                                                                                                                                                                                         2604 TyrCysIleCysLysThrProTyrAspGluSerLysPheTyrIleGlyCy
                                                                                                                                                                                                                                                                                                                                                                                                                                     compounds binding to it and acting as agonists or antagonists, which are potentially useful for the treatment and prevention of cancer and other cell proliferation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              containing a bromo domain. The factor interacts with proteins involved in the chromatin-mediated transcription regulatory mechanism. It binds to hSNF2H, hSNF2L and NCOA-62/Skip. It can be used for screening
                            22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a human transcriptional regulatory factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 139-151; 154pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcriptional regulatory factor containing a bromo domain TCoAl encoding it
                                                                                                                                                                              55 CGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                   5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
                                                                                                                                                     sAspArgCysGlnAsnTrp
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transcriptional regulatory factor SEQ
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60.870
                                                                                  Protein; 2907 AA
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transdik
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KW Protein sasay; genetic mapping;
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CS Arabidopsis thaliana.
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PN termination sequence.
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PN termination sequence.
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                                                                                 Protein identification; signal transduction hybridisation assay; genetic mapping; gene \varepsilon termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a human transcriptional regulatory factor containing a bromo domain. The factor interacts with proteins involved in the chromatin-mediated transcription regulatory mechanism. It binds to hswr2H, hswr2L and NCOA-62/Skip. It can be used for screening compounds binding to it and acting as agonists or antagonists, which are potentially useful for the treatment and prevention of cancer and
                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ
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N-PSDB; AAZ39032.
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bromo-domain; cell proliferation;
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Gaps: 0
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                                                                                                    mapping; gene expression control; promoter;
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cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 include: cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC/7607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in Example of activities
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TyrCysIleCysArgGlnProHisAsn..
                                         TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
                                                                                                                                                                                 Similarity:
                                                                                                                                                                                                                                                                                                                                             present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombolytic; cardiovascular disorder; infection; disease; drug screening.
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3.531
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  .AsnArgPheMetIleCysCy
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                                                                                 181
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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAY67579
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AAY67579 standard; Protein;
                                                 The invention provides nucleic acids encoding the human and murine death inducer-obliterator 1 (DIO-1) polypeptides. The polypeptides can be expressed by standard recombinant methodology. The DIO-1 polypeptides, agonists and antagonists are used as a medicament for treating diseases characterized by an alteration in cell death or by hyperproliferation, e.g. cancer, autoimmune diseases, diabetes, rheumatoid arthritis, benign e.g. cancer, autoimmune diseases, diabetes, rheumatoid arthritis, benign tumours, malignant tumours or hyperproliferative skin disorders. They are
                                                                                                                                                                                               New DNA encoding human and murine death inducer-obliterator 1 polypeptides, useful in the treatment of cancer, autoimmune diseases diabetes, rheumatoid arthritis, benign tumors, malignant tumors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Death inducer-obliterator 1; DIO-1; cell death; cancer; tumour; autoimmune disease; cytostatic; immunosuppressive; antidiabetic; antirheumatic; antiinflammatory; antiproliferative.
Sequence
                                      also useful
                                                                                                                                                           Claim
                           conditions. The
                                                                                                                                                                                    hyperproliferative skin disorders
                                                                                                                                                                                                                                                     N-PSDB;
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17-SEP-1998;
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DB; AAZ90578.
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  AA;
                          the treatment of metabolic, proliferative or inflammatory e present sequence represents the human DIO-1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                              98SE-0003069.
98US-0100873.
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271..288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence"
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                                                                                                                                                                                                                                                                                             Martinez
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alignment\_scores:

Quality: Ratio:

56.50 3.531 69.565

Percent

Identity: Length:

39.130

Percent Similarity:

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seq_documentation_block:
ID AAB93638 standard; Pr
XZ AAB93638;
XZ AAB93638;
XX PT 26-JUN-2001 (first e
XX Human protein sequenc
XX Human; primer; detect
XX Human; primer; detect
XX Human; primer; detect
XX Homo sapiens.
XX EP1074617-A2.
XX 29-JUL-1999; 99JP---
PR 27-AUG-1999; 99JP---
PR 27-AUG-1999; 99JP---
PR 27-AUG-1999; 99JP---
PR 27-AUG-1999; 99JP---
PR 17-AUG-1999; 99JP---
PR 27-AUG-1999; 99JP---
PR 27-AUG
The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of CC cliponucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence complementary to a CC oligonucleotide comprises a 3'-end sequence, where the CC oligonucleotide comprises a 1 least 15 nucleotides and the combination of CC the 5'-end sequence', 3'-end sequence is selected from those defined in CC in gene therapy. The primers set useful for synthesising polynucleotides, CC oparticularly full-length cDNAs. The primers are useful for synthesising polynucleotides, CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs and methods. AAH03166 to AAH13628 and
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US-09-684-016-48411 x AAY67579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB93638 standard; Protein; 562
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Sugiyama T, Wakamatsu
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2000JP-0183767.
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A, Nagai K,
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Otsuki
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                                                                                                                                                                                                                                                                                                                                                                   Death inducer-obliterator 1; DIO-1; cell death; cancer; tumour; mouse; autoimmune disease; cytostatic; immunosuppressive; antidiabetic; antirheumatic; antiinflammatory; antiproliferative.
                                          N-PSDB;
                                                                          Alonso CM,
                                                                                                                                                                   10-SEP-1999;
                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                               Murine death
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17-SEP-1998;
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                                                                                                (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES
(BANN/) BANNERMAN D G.
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                                          2000-271426/23
DB; AAZ90579.
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98US-0100873
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/note= "zinc finger motif"
290..315
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                                                                           Martinez
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New DNA encoding human and murine death inducer-obliterator 1 polypeptides, useful in the treatment of cancer, autoimmune diseases, diabetes, rheumatoid arthritis, benign tumors, malignant tumors and

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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides nucleic acids encoding the human and murine dea inducer-obliterator I (DIO-1) polypeptides. The polypeptides can be expressed by standard recombinant methodology. The DIO-1 polypeptides, agonists and antagonists are used as a medicament for treating disease characterized by an alteration in cell death or by hyperproliferation, e.g. cancer, autoimmune diseases, diabetes, rheumatoid arthritis, beni
                                                                                                                                                                                                                                                                                                                          5-oxoprolinase; rat;
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAW61369 standard; Protein; 1288 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Fig 1D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyperproliferative skin disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sAspArgCysGluGluTrp 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrCysIleCysArgGlnProHisAsn...AsnArgPheMetIleCysCy 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqp/AA1998.DAT: AAW61369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
               CORNELL RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            614 AA;
                                      96US-0762428
                                                             97WO-US22851
                                                                                                                                                                                                                             /note=
698
                                                                                                                                                                                                    /note=
919
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3.531
69.565
                                                                                                                                                    /note=
1106
                                                                                                                                                                              1003
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                                                                                                                                                                                       note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27pp; English.
                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                          glutathione;
                                                                                                                                       "putative N-glycosylated"
                                                                                                                                                                                                              "putative N-glycosylated"
                                                                                                                                                                                       "putative
                                                                                                                                                              "putative N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity:
                                                                                                                                                                                       N-glycosylated"
                                                                                                                                                                                                                                                                                                                     5-oxoprolinuria; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
: 1
: 39.130
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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1997.DAT:AAW18030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAW61369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This polypeptide comprises rat 5-oxoprolinase, an enzyme that catalyses the ATP dependent cleavage of 5-oxoproline to L-glutamate in the metabolism of glutathione. The amino acid sequence is deduced from a cDNA sequence (see AAV28112) derived from overlapping clones from a rat kidney cDNA library. The invention is directed toward isolated nucleic acid molecules encoding mammalian toward isolated nucleic acid molecules encoding mammalian comprolinase (mSOP). Deficiency of this enzyme is associated with 5-oxoprolinuria. Expression vectors and host cells comprising the nucleic acid molecules are provided, as well as methods of increasing (by gene therapy) or decreasing (e.g. using antisense or ribozyme molecules) the expression of mSOP in host cells. The invention also provides a method of screening a substance for its ability to modify mSOP function, and a method for isolating other mSOP molecules. DNA probes and primers, and antibodies specific for mSOP are provided, each of which can be used to detect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-684-016-48411/rev x AAW61369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 HisValSerLeuSerSerGluValMetProMetValArgIleValProAr 231
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N-PSDB; AAV28111-12.
       (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                             Huntingtin interacting protein; HIP1; Huntington's disease;
                                                                                                                                                                                                                                                                 Huntingtin interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 gGlyHisThrAlaCysAlaAspAlaTyrLeuThrProThr 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 49-55; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalian 5-oxoprolinase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating 5-oxoprolinuria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breslow E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 AGGTCATCAGGGTTGTAAGGCATCTCACATTTACAATACC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 CATGTGAAACTTACCAGTCAGTGCAGCCCT.....CGCATTGCGCCCATT 43
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                                                                                                                                                                                                                                                                                                    (first entry)
                                       95US-0006882.
                                                                         96WO-US18370
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2.800
66.667
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                                                                                                                                                                                                                                                                   HIP1
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Gaps:
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seq_documentation_block:
ID AAY59269 standard; Pr
XX AC AAY59269;
XX 17-APR-2000 (first e
XX 17-APR-2000 (first e
XX Huntingtin Interactir
XX Huntingtin Interactir
XX Huntingtin's disease;
XX Huntington's disease;
XX Homo sapiens.
XX Wo9960986-A2.
XX WO9960986-A2.
XX PPN W09960986-A2.
XX XX PPD 02-DEC-1999; 99WO-U
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US-09-684-016-4
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAW18030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-684-016-48411/rev x AAW18030
                                                                                                                                                                                                   Huntingtin Interacting Protein; HIP; death effector domain; DED; human; apotosis; HIP-apoptosis modulating protein; cell death; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of huntingtin into brain cell membranes. Its amino acid sequence was deduced from a human frontal cortex cDNA clone (AAT67187). The effects of HD in a patient expressing huntingtin protein with an expanded polyglutamine tract can be ameliorated by increasing the amount of expressed HIPl in the brain using gene therapy approaches. Modified forms of HIPl which bind more effectively to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                                                                           Human huntingtin-interacting protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 28-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding Huntington's disease interacting protein - useful ameliorate effects of disease in patient expressing Huntingtin protein with expanded CAG repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expanded HD protein can be used to convert the expanded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCACATTTACAAT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a functional molecule.
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                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                              disease; nootropic; anticonvulsant; cytostatic;
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        99WO-US11743.
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2.077
68.421
                                                                                                                                                                                                                                                                                                                                                                                  Protein; 914
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                                                                                                                                                                                                                                                             (HIP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.842
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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAY59270
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                                                                                                                                                                                                                      documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to Huntingtin Interacting Protein (HIP), that includes a death effector domain (DED), suggesting apototic function. Proteins with DED (referred as HIP-apoptosis modulating proteins) are useful for inducing apoptotic death in cells. The HIP is a logical target for therapy in Huntington's disease since it has a differential apoptotic activity, modulated by interaction with Huntingtin having normal and expanded repeats. HIP is also used as therapeutic agent to introduce apoptosis in cancer cells. Increasing expression of normal (non-expanded) Huntingtin or the HIP-apoptotic modulator-binding portion, a modified HIP-apoptotic modulator in which the DED has been deleted, is helpful for
                                                                                                               Human huntingtin-interacting protein
                                                                                                                                               17-APR-2000
                                                                                                                                                                                                                                                                                 110
                                                                                                                                                                           AAY59270;
                                                                                                                                                                                                         AAY59270 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  techniques, and cancers
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MERCK FROSST CANADA INC.
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                                                                                                                                              (first entry)
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JP, Raspe
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2.077
68.421
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DM;
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36.842
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Huntingtin Interacting Protein; HIP; death effector domain; apotosis; HIP-apoptosis modulating protein; cell death; gene Huntington's disease; nootropic; anticonvulsant; cytostatic

cytostatic;

gene

therapy;

chromosome 7q11.23.

Homo sapiens

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KW XXX DE XXX XXX Seq.
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US-09-684-016-48411/rev x AAY59270
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                                                                                                                                                           documentation_block:
             Human;
foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to Huntingtin Interacting Protein (HIP), that includes a death effector domain (DED), suggesting apototic function. Proteins with DED (referred as HIP-apoptosis modulating proteins) are useful for inducing apoptotic death in cells. The HIP is a logical target for therapy in Huntington's disease since it has a differential apoptotic activity, modulated by interaction with Huntingtin having normal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYBR-)
(MERI )
                                                                                     10-AUG-2001
                                                                                                                 AAE03341;
                                                                                                                                                                                                                                                                           271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity, modulated by
 immune
                                                     Human gene 17 encoded secreted protein HTOIZ28, SEQ ID NO:115
                                                                                                                                              AAE03341 standard;
                                                                                                                                                                                                                     286
                                                                                                                                                                                                                                                                                                                                    255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expanded repeats. HIP is also used as a therapeutic agent to introduce apoptosis in cancer cells. Increasing expression of normal (non-expanded) Huntingtin or the HIP-apoptotic modulator binding portion, a modified HIP-apoptotic modulator in which the DED has been deleted, is helpful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          techniques, and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vallaincourt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalchman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-1999
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                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                                                                      69 TCAGTGCAGCCCTCGCATTGCGCCATTAGGTCATCAGGGTTGTAAGGCAT
                                                                                                                                                                                                                  erHisLeuTyrAsp
                                                                                                                                                                                                                                               CTCACATTTACAAT
                                                                                                                                                                                                                                                                          yGlnCys.....ArgLeuAlaProLeuIleGlnValIleLeuAspCysS
                                                                                                                                                                                                                                                                                                                                  ValPheAsnSerLeuAspMetSerArgSerValSerValThrAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                             GTGTGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-097055/08
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system
           secreted protein; proliferative disorder; cancer; tumour; abnormality; developmental abnormality; haematopoietic di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNIV BRITISH COLUMBIA.
MERCK FROSST CANADA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huntington's disease.
                                                                                                                                                                                                                                                                                                                                                                                         to: AAY59270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1090 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayden MR,
JP, Rasper
                                                                                    (first entry)
disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57-62; 91pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0085199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US11743
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2.077
68.421
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                                                                                                                                                                                                                     290
                                                                                                                                                                                                                                               σ
                                                                                                                                              Protein;
AIDS; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hackam A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the human
                                                                                                                                                                                                                                                                                                                                                                                       to: 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chopra V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           38
1
36.842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicholson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease
rheumatoid arthritis
                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy
             disorder;
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gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used
                                                                                                                                                                                                                                                                                                                                proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune syst AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD07705-AAD07759 represent cDNAs corresponding to 19 human secreted protein genes, and AAE03392-AAE03346 represent the proteins they encode. AAE03347-AAE03375 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the
                                                       as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used i alleviating symptoms associated with the disorders mentioned about the contract of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding human secreted preventing, treating or ameliorating a disorder, e. Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1999; 99US-0164750.
30-JUN-2000; 2000US-0215128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2000; 2000WO-US30674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endocrine disorder; infection; wound healing; vulnerary;
cell culture; chemotaxis; food additive; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkinson's disease; cognitive disorder; schizophrenia; asthma
skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
cardiovascular disorder; angiogenic disorder; kidney disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200134800-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gastrointestinal disorder; pregnancy-related disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       penes, based on the tissues in which they are most highly expressed, include developing products for the diagnosis or treatment of iferative disorders, cancer, tumours, foetal and developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-329085/34
)B; AAD07754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 494; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Komatsoulis GA,
   assay (ELISA).
immunoassays e.g., radioimmunoassay assay (ELISA). The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
120
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32..132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human_mature_secreted_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĭ
   represents
                                  or enzyme linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins, used
.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system,
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and
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Soxco

secreted protein of the invention

132 AA;

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seq_documentation_block:
ID AAE03308 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                             foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder;
               (HUMA-) HUMAN GENOME SCI INC
                                             12-NOV-1999; 99US-0164750.
30-JUN-2000; 2000US-0215128.
                                                                                                                                                                                                                                                                                                                                                               gastrointestinal disorder; pregnancy-related disorder;
endocrine disorder; infection; wound healing; vulnerar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 TGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAA...
                                                                                             08-NOV-2000; 2000WO-US30674.
                                                                                                                                17-may-2001
                                                                                                                                                                WO200134800-A1
                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                binding partner identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE03308 standard; Protein; 143 AA
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                                                                                                                                                                                                                                                                                                                                                 culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  secreted protein; proliferative disorder; cancer; tumour; abnormality; developmental abnormality; haematopoietic di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoded secreted protein HTOIZ28, SEQ ID NO:82
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2.058
50.980
                                                                                                                                                                                           /label= Signal_peptide
32..132
/label= Human_mature_secreted_protein
                                                                                                                                                                                                                                                               Location/Qualifiers
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seq\_documentation\_block:

83 14 99

ATT ::: Leu

99

seq\_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAY36128

rAsnCysSerLeuValProGlyValValAlaHisThrCysAsnProLysV

83

al...ProLeuGlyLeuGlnGlyCysGluLeuProCysProAlaGluHis

66

TCAGTGCAGC.....

.....CCTCGCA 53

116 TGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAA...

CTTACCAG

66

50 TrpAsnIleLeuLeuTyrSerValGlySerLysValSerGlyLeuCysSe

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alignment_block:
                                                                                                                                                                      alignment_scores:
Align seg 1/1
                                          US-09-684-016-48411/rev x AAE03308
                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                  skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodles specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diamnoscasay or enzyme linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 19 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                 in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein genes, and AAE03292-AAE03346 represent the proteins they encode.
AAE03347-AAE03375 represent human secreted protein fragments or variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD07705-AAD07759 represent cDNAs corresponding to 19 human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 467-468; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben
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DB; AAD07721.
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  to: AAE03308
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50.980
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Percent Identity:
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to:
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  143
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alignment_block:
US-09-684-016-48411 x AAY36128
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Quality:
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                                                                                                                                                                                                                                                                   Ratio:
Percent Similarity:
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17-DEC-1997;
09-FEB-1998;
13-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                             or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes corresponding to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein; human; cytokine; cellular proliferation; cell movems cellular differentiation; immune system regulator; anti-inflammatory; haematopoiesis regulator; tissue growth regulator; tunour inhibitor; reproductive hormone regulator; chemotaxis; chemokinesis; gene therap;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
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  85
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                                                                                  69
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uPheLeuTyrLeuSerAlaGluTyrSerThrLys
                                     AAGGTGATACTTATCTTCAATTTATTCCACACAA 121
                                                                         {\tt AspIleThrAlaAspLeuGluAsnIlePheAspTrpAsnValLysGlnLe}
                                                                                                                      GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGT
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98US-0081563
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97US-0069957
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                                                                                                                                                                                                                                       seq_documentation_block:
ID AAB24029 standard; Pr
AC AAB24029;
XX
DT 25-JAN-2001 (first e
XX Human PRO3567 protein
XX
Human; tumour; diagnc
KW identification; tumou
XX
Homo sapiens.
XX
PN WO200053750-A1.
XX
PN WO200053750-A1.
XX
PP 01-SEP-1999; 99WO-1
PR 01-SEP-1999; 99WO-1
PR 01-DEC-1999; 99WO-1
XX
PI DEC-1999; 99WO-1
XX
ANTIBODIE ACCUMENTECH INC
PI Horoxida activity
XX
Claim 61; Fig 18; 22:
XX
CC The present invention
CC The present invention
CC PRO3434; PRO1927; PR
CC The present incomplex fo
CC Cells. Increased exp
CC cells. AAC58103
CC probes used in examp
CC probes used in examp
CC probes activity by inducic
CC probes activity by inducic
CC probes as AAC58103
CC probes as AAC58103
CC probes activity accuments activity by inducic
CC probes activity by induc
                  Align seg 1/1
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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAB24029
AAB24029 standard; Protein; 180
Å
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(first entry)
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protein sequence SEQ ID NO:27 diagnosis; neoplastic disease;
; tumourigenesis; anticancer; d detection proliferation;

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GENENTECH INC
                         99US-0162506.
99WO-US28313.
99WO-US28634.
                                                                                                           99WO-US28551
                                                                     99WO-US20111
                                                                                99WO-US05028
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Goddard ۶ Gurney ΑL, Roy MA, Watanabe CK, Wood

W,

Antibodies specific for PRO polypep the growth of tumors in mammals, an polypeptide activity or expression PRO polypeptides, used to diagnose amammals, and to identify inhibitors expression and s of inhibit

226pp; English.

The present invention describes an antibody that binds to a human control of the protein (I) selected from: PRO381; PRO1295; PRO1410; PRO1755; PRO1780; PRO434; PRO1927; PRO3567; PRO1295; PRO1295; PRO1395; PRO1395; PRO13944; PRO4344; PRO4344; PRO4397; PRO4407; PRO1555; PRO1295; PRO1293; and PRO2262. (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AAC58019 to AAC58102 represent invention for human PRO sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human PRO sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human protein sequences given in the exemplification of PRO polynucleotide and protein the present invention.

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alignment_block:
                                                         alignment_scores:
US-09-684-016-48411 x AAB24029
                            Percent Similarity:
                                               Quality:
                                    Ratio:
                            53.00
2.650
71.429
                             Percent
                             Identity:
                                     Gaps:
                             42
                             28
0
. 857
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38 GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGT

to: AAB24029 from: 1

to:

180

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AC AAB43274 standard; Protein; 601 AA
AC AAB43274;

XX AAB43274;

XX AAB43274;

XX DT 08-FEB-2001 (first entry)

XX Human; open reading frame; ORFX; d

XX Vulnerary; antipsoriatic; antipark

XX ANDA3274;

XX ANDA3374;

XX ANDA
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                                    AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORRX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID, AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal hæmoglobinuria; burn; wound; pone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 5260-5262; 5507pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAB43274
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            neurodegenerative disorders,
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            osteoarthritis
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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAY60285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobiuria, antiinflammatory disease; to enhance
                                                                           New nucleic acid sequences expressed in uterine cancer tissues, derived polypeptides, for treatment of uterine and endometrial and identification of therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 23; Page 412; 444pp; German.
                                                                                                                                N-PSDB;
                                                                                                                                            WPI; 1999-591957/51.
                                                                                                                                                                                                                                                  17-APR-1998;
                                                                                                                                                                                                                                                                                                     DE19817948-A1
                                                                                                                                                                                                                                                                                                                                                                    Endometrium; human;
                                                                                                                                                                                                                                                                                                                                                                                            Human endometrium tumour EST
                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY60285 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 SerSerLeuLysSerTyrIleLeuIleHisGlnLysTrpThrIleCysCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                     Rosenthal A,
                                                                                                                                                                                             (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                        17-APR-1998;
                                                                                                                                                                                                                                                                           21-OCT-1999
                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     treatment; uterine;
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                                                                                                                                                                     Specht T,
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52:174
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                                                                                                                                                                                                                                                                                                                                                      gene therapy; expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                    tumour; cancer; anticancer; cytostatic; EST:
                                                                                                                                                                      Hinzmann
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                                                                                           cancer
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This invention describes novel human nucleic acid (cDNA) sequences that are highly expressed in uterine tumour tissue and which have

cytostatic activity. (A) are used (i) for recombinant

anticancer and

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seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAX59941-Y60328 represent protein fragments encoded by the human endometrium tumour cDNA library derived EST fragments represented in AAX41981-Z42121.
                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori cell envelope transporter protein 13726562.aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW20131 standard; Protein; 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 AAATTGAAGATAAGTATCACCTTACATGTG.....AAACTTACCAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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95US-0487032
                                                                                                                                                                    96WO-US09122
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                                                                                                                                                                                                                                                                         /label= unknown
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seq_documentation_block:
ID AAW20619 standard; Pr
XX
AC AAW20619;
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T14-JUL-1997 (first e
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DF 14-JUL-1997 (first e
XX
Cytoplasmic; vaccine;
KW cytoplasmic; vaccine; bindi
KW bacteria; inhibitor;
KW diagnosis.
XX
Helicobacter pylori.
XX
PN W09640893-A1.
XX
PD 19-DEC-1996.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-1
XX
PF 07-JUN-1995; 95US-1
XX
PR 01-APR-1995; 95US-1
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PA (ASTR ) ASTRA AB.
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PI Berglindh OT, Smith
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US-09-684-016-48411/rev x AAW20131
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                                                                                                                                                                                                                                                                                                                  Cytoplasmic; vaccine; prevention; identification; binding compound; bacteria; inhibitor; duodenal ulce
                                                                                                                                                                                                                                                                                                                                                                                               H. pylori transporter protein,
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                                                                                                                                                                                                                                                            Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 56; Page 356; 1481pp;
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95US-0487032
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61.290
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                                                                                                                                                                                                                                                                                                                      duodenal ulcer
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                                                                                                                                                                                                                                                                                                                                      bacterium;
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                                                                                                                                                                                                                                                                                                                    acterium; life cycle; activa
disease; chronic gastritis;
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Smith D,

Mellgaerd BL;

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alignment_block:
US-09-684-016-48411/rev x AAW20619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a H. pylori transporter protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, infection or to identify H. pylori polypeptide binding compounds, is seful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from converlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant chomology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                            Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                  Align seg 1/1 to: AAW20619 from: 1 to: 377
                                                                                       60 CCCTCGCATTGCGCCATTAGGTCATCAGGGTTGTAAGGCATCT 18
::::|||||| :::|||||:::||||||
190 yGlnLysIleAlaLeuIleGlyHisSerGlyCysGlyLysSer 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 56; Page 1045-46; 1481pp; English.
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N-PSDB; AAT67872.
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2.684
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Gaps: 0
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COMM. DEP 115-08-608 - 1.  
COMM. DEP 115-08-74-10-25-0 + 50.00 115-02 15-82 244  
COMM. DEP 115-08-74-10-25-0 + 50.00 115-04 18-0 47  
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COMM. DEP 115-08-74-10-25-0 + 50.00 115-04 18-0 47  
COMM. DEP 115-08-10-28-10-28-10-28-10-28-10-24-11-24-1 48-0 0 115-04 18-0 47  
COMM. DEP 115-08-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-10-28-1
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Database length: 22503292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search time (sec): 25.790000
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-QB=!ssued_Patents_AA -QPMT=fastan -SUFFIX-std.rai
-GAPOP=12.000 -GAPOEXT=4.000 -MINMATCH+0.100 -XAPOPEL=0.000
-LOODEXT=0.000 -GAPOP=4.500 -GGAPOXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPOXT=7.000 -YGAPOP=10.000
-YGAPOXT=0.500 -FGAPOP=6.000 -FGAPOXT=7.000 -YGAPOP=10.000
-YGAPOXT=0.500 -DELOP=6.000 -DELOXT=7.000 -YGAPOP=10.000
-YGAPOXT=0.500 -DELOP=6.000 -DELOXT=7.000 -YGAPOP=10.000
-THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=pfs -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09684016_@CGN1_1_0 -NCPU=6 -ICPU=3 -LONGLOG
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                                                                                                                                                                                   seq_documentation_block:
; Sequence 4, Application US/09085199B
; Patent No. 6235879
                                                                                                                                                                                                                                                                                                                                      seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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; TYPE: amino acid
; STRANDEDNESS: not
; TOPOLOGY: linear
; MOLECULE TYPE: prote
US-08-762-428A-6
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-345-212-14-
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-09-249-003-14-
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-483-2+
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-483-5+
                                                                                                                                                                                             Align seg 1/1 to: US-08-762-428A-6 from: 1 to: 1288
                                                                                                                                                                                                                                      US-09-684-016-48411/rev x US-08-762-428A-6
                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 716-263-1600 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,10
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ye, Guo-jie
APPLICANT: Breslow, Esther M.
APPLICANT: Meister, Alton
TITLE OF INVENTION: 5-OXOPROLINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1288 amino acids
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MEDIUM TYPE: Floppy disk
                                      231 gGlyHisThrAlaCysAlaAspAlaTyrLeuThrProThr 244
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                                                                         42 AGGTCATCAGGGTTGTAAGGCATCTCACATTTACAATACC 3
                                                                                                                                                      86 CATGTGAAACTTACCAGTCAGTGCAGCCCT.....CGCATTGCGCCATT
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TELEPHONE: 716-263-1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/762,428A
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-085-199B-4
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5. 6120993
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Percent Identity:
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seq_documentation_block:
; Sequence 5, Application US/09085199B
; Patent No. 6235879
                                                                                            seq_name:
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US-09-085-199B-4
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TELEFAX: (970) 668-2052

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 914
TYPF:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-085-199B-4 from: 1 to: 914
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: LATSON, MARINA T.
REGISTRATION NUMBER: 32038
REFERENCE/DOCKET NUMBER: UB
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Oppedahl & Larson
STREET: PO Box 5270
                                                                                                                                    110
                                                                                                                                                                                                                                                                                                                       119 GTGTGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTACCAG 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                69 TCAGTGCAGCCCTCGCATTGCGCCATTAGGTCATCAGGGTTGTAAGGCAT 20
                                                                                                                                                                                                                                                                                     79 ValPheAsnSerLeuAspMetSerArgSerValSerValThrAlaAlaGl 95
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TOPOLOGY: linear
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                                                                                                                                                                       CTCACATTTACAAT 6
                                                                                                                                                                                                            yGlnCys.....ArgLeuAlaProLeuIleGlnValIleLeuAspCysS 110
                                                                                            /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-085-199B-5
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Chopra, Vikramjit Singh
Kalchman, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 36.842
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seq_documentation_block:
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US-09-684-016-48411/rev x US-09-085-199B-5
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    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION:
US-09-085-199B-5
                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-549-515-9
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                                    Sequence 9, Application US/08549515 Patent No. 6054123
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (970) 668-2052
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: no
ORIGINAL SOURCE:
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REGIRAL STATES AND S
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                            271 yGlnCys.....ArgLeuAlaProLeuIleGlnValIleLeuAspCysS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 ValPheAsnSerLeuAspMetSerArgSerValSerValThrAlaAlaGl 271
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ADDRESSEE: Oppedahl & Larson
                                                                                                                                                                                                                                                                                     286 erHisLeuTyrAsp 290
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                                                                                                                                                                                                                                                                                                                          19 CTCACATTTACAAT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/085,199B FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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SOFTWARE: WordPerfect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Hackam, Abigail
Huq, A.H.M. Mahbubul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chopra, Vikramjit Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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2.077
68.421
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Percent Identity:
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TITLE OF INVENTION:

Dimethylsulphoxide Reductase Enzyme

Haemophilus Influenzae

Klein, Michel H

Loosmore, Sheena M

NUMBER OF SEQUENCES: 1

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-866-545-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                 Sequence 4,
                                                                                                                                                                                                                     sequence 4, Application US/08866545
Patent No. 6265535
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                           119 rLysGlyHisMetThrLysCysAspGlyCysTyrAsp 131
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LENGTH: 207 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                     103 ArgTyrCysHisMetAlaCysProTyrGlyAlaProGlnTyrAsnGluTh 119
                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                 44 .....ATGGCGCAATGCGAGGGCTGCACTGAC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AGGTATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 27-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Suite CITY: Toronto
                                   ADDRESSEE:
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New York
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Suite 701, 330 Unviersity Avenue
             1155 Avenue of the Americas
                                                                                                                                                                 Takasaki,
                                                                                                                                                                                       Murali,
                                                                                                                                                                                                     Greene, Mark I.
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                                   Pennie &
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3.400
51.724
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27
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                                                                                                                                                                     Wataru
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                                   Edmonds LLP
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Gaps: 1
Percent Identity: 34.483
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; MOLECULE TYPE: US-08-866-545-4
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                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08232087A Patent No. 5866372
                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Stein, Harald
APPLICANT: Drkop, Horst
APPLICANT: Latza, Ute
TITLE OF INVENTION: Lymphoid CD30-Antigen
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650-493-4935
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                                                                                                                                                                                                                                                                                                                                                                                                   60 uAlaCys 62
                                                                                                                                                                                                                                                                                                                                                                                                                                    58 GGGCTGC 64
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                                                                                                STREET: 8110 Gateho
CITY: Falls Church
STATE: Virginia
                                                                      ZIP:
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REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 30-MA
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                                                                                     COUNTRY:
                                                                                                                                                      ADDRESSEE:
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                                                                                                                                    E: Birch, Stewart, Kolasch & Birch, LLP
8110 Gatehouse Road, Suite 500 East
                                                                                 U.S.A.
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4.167
63.158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 19
: 0
: 36.842
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alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6,
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LENGTH: 159 amin.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                 APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 uAlaCysSer 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 GGGCTGCACT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 CysArgCysAlaTyrGlyTyrTyrGlnAspGluThrThrGlyHisCysGl 93
                                                                                                                                                                                                 AUDRESSEE: James W. Hellwege STREET: P.O. Box 2266 Eads Station CITY: Arlington.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 08-SEI CLASSIFICATION: 43
                                                                                                                                                     COUNTRY: UZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..159
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein LOCATION: 1..159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                        Virginia
                                                                                                                                                                      USA
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65.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "NGFR, see Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/232,087A
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-477-347-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 51
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                           APPLICATION NUMBER: IL 10
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                  FILING DATE: PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polo---
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                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                STREET: 419 Sever CITY: Washington
NAME: Townsend, G. REGISTRATION NUMBER:
                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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FILING DATE: 22-APR-1992
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BIGDA, Jacek
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BELETSKY, Igor
                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
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                G. Kevin
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                                                                     IL 106271
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Percent Identity: 36.842
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-477-347-15
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US-09-684-016-48411 x US-08-477-347-15
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Percent Similarity:
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                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
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SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
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APPLICANT: WALLAC
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                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: METT, IGOR
APPLICANT: ENGELMANN, Hartmut
TITLE OF INVENTION: TNF INHIBITORS
                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BIGDA, Jacek
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                                                                                                                                                                                                      APPLICATION NUMBER: US/0: FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 419 Seven
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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419 Seventh Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BELETSKY, Igor
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linear
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IL 90339
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Gaps: 0
Percent Identity: 36.842
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; LENGTH: 159 amino
; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: pepti
US-08-476-862-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-468-560C-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08468560C Patent No. 6270998
              TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
                                                       REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/468,560C FILING DATE: 06-JUN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: ITOH, Naot
APPLICANT: YONEHARA,
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GGGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. BOX 7:
CITY: FALLS CHURCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O. BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                 MURPHY JR., GERLAD M
                                                                                                                                                                                                                                                                                                                                                         22040-0747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAGATA, Shigekazu
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Gaps: 0
Percent Identity: 36.842
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TYPE: amino acid STRANDEDNESS: si

single

amino acids

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alignment_scores:
Quality:
Ratio:
                                                                               ; TOPOLOGY: 1; MOLECULE TYPE: US-08-974-022-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-974-022-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: !
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
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                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 12-DE
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                 LENGTH:
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o. 6015938
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Lacey, David L.
Calzone, Frank J.
Chang, Ming-Shi
                                                                                                                                                         224 amino acids
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Gaps: 0
Percent Identity: 36.842
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Length:
Gaps:
     19
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alignment_block:
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                                                                       Align seg 1/1 to: US-08-795-445A-50
                                                                                                           US-09-684-016-48411 x US-08-795-445A-50
                                                                                                                                                                 Percent Similarity:
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 50
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TOPOLOGY: lin
MOLECULE TYPE:
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STATE: California
107 CysArgCysAlaTyrGlyTyrTyrGlnAspGluThrThrGlyArgCysGl 123
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APPLICATION NUMBER: (
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                8 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/795,445A
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linear
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    Sequence 50, Applicati
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                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-974-186-50
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                                                                 Sequence 50, Application US/08974186
Patent No. 6284740
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 50:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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CORRESPONDENCE ADDRESS:
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                                      APPLICANT:
                                                                                                                                                                                             123 uAlaCys 125
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T: One Amgen Center Drive
Thousand Oaks
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Lacey, David L.
Calzone, Frank J
Chang, Ming-Shi
Boyle, Willaim J.
Lacey, David L.
Calzone, Frank J.
Chang, Ming-Shi
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Gaps: 0
Percent Identity: 36.842
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US-08-974-186-50
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Percent Similarity:
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                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                            Sequence 50,
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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STATE: California
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NAME: Winter, Robert B.
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NUMBER OF SEQUENCES:
                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                               TITLE OF INVENTION:
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7TD: 91320-1789
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP:
           COUNTRY:
                                                                                ADDRESSEE:
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91320-1789
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6288032
                            California
                                                           E: Amgen Inc.
1840 Dehavilland Drive
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                                                                                                                                                                             Lacey, David L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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63.158
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                                                                                                                                                              Frank J.
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                                                                                                                               OSTEOPROTEGERIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              to:
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0
36.842
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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alignment_block:
US-09-684-016-48411 x US-08-795-446B-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. GENERAL I
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equence 1, App-
-+ No. 5948641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: prote
                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La1, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: METAL RESPONSE ELEMENT BINDING PROTEIN
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 CysArgCysAlaTyrGlyTyrTyrGlnAspGluThrThrGlyArgCysGl 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 GGGCTGC 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TORNEY/AGENI IN.

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A
REFERENCE/DOCKET NUMBER: 50:
                                                                                         APPLICATION NUMBER:
FILING DATE: Herewi
                                                                                                                                                                                                                                                                             STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/795,446B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                           94304
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                                                                                                                                                                                                                                                                                                                 3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 amino acids
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                                                                                                                                                                                    IBM Compatible
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                                                                                          Herewith
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                                                                                                            US/08/864,804
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36.842
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seq_documentation_block:
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Quality:
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US-08-864-804-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09086483A Patent No. 6214580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE UTITALITY
              ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                   CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 TyrCysTyrCysGlyGlyProGlyGluTrpAsnLeuLysMetLeuGlnCy 205
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 sArgSerCysLeuGlnTrp 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILL
LIBRARY: Live
TONE: 2048959
                                                               FILING DATE: DE CLASSIFICATION:
                                                                                                                                 FILING DATE: May-30-97 CLASSIFICATION: 435
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                                                                                                                                                                                                                    FILING DATE: May-29-98
                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                          20850
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                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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10 KEY WEST AVENUE
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60.870
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NUMBER:
                                                                                                                                                                                                                                      US/09/086,483A
                                                                                                                                                                                                                                                                     Release #1.0, Version
                                                                                                                                                                   60/050,936
                                                                                                  60/069,112
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39.130
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-086-483A-4
; MOLECULE TYPE: protein US-09-041-886-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-041-886-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09041886 Patent No. 6235872
                                                                      TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (301) 309-8439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acid
                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                      TOPOLOGY: 1:--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 GGGCTGC 64
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CITY: San Diego
STATE: California
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                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA 57
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63.158
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Percent Identity: 36.842
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alignment_block:
us-09-684-016-48411 x us-09-006-353A-5
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; MOLECULE TYPE:
US-09-006-353A-5
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US-09-684-016-48411 x US-09-041-886-2
                                                                                                                                   alignment_scores:
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Align seg 1/1 to: US-09-006-353A-5 from: 1 to: 427
                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-09-041-886-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09006353A Patent No. 6261801
                                                                                                                                                                                                                                                                                        TELEFAX: (301) 309-851 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 CysArgCysAlaTyrGlyTyrTyrGlnAspGluThrThrGlyArgCysGl 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 GGGCTGC 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                     Quality:
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                                                                                                                                                                                                                                                                       427 amino acids
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RUBEN, STEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEI, YING-FEI
YU, GUO-LIANG
                                                                                                                                                                                                                        linear
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63.158
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Gaps: 0
Percent Identity: 36.842
                                                                                   Gaps:
Percent Identity:
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alignment_block:
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; MOLECULE TYPE:
US-08-553-436A-8
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                                                                               Align seg 1/1 to: US-08-553-436A-8
                                                                                                                    US-09-684-016-48411/rev x US-08-553-436A-8
                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08553436A Patent No. 5866790
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 382-080
TELEX: 236925
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HESSE, Holger
APPLICANT: MULLER-ROBER, Bernd
TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE
TITLE OF INVENTION: CONCENTRATION
399 GluAspLysTyrHisPheSerCysGlnPheSerAlaAspLeuMetAlaMe 415
                                SEQUENCE CHARACTERISTICS
LENGTH: 766 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: DE P
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: P/951-117
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FILING DATE: 20-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/01 FILING DATE: 17-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 382-0700
                                                                                                                                                                                                                                                                                                                     protein
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24-MAY-1993
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2.273
38.596
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                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                              TOPOLOGY: unknown MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/364,379 FILING DATE: 12-JUN-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/930,462 FILING DATE: 20-AUG-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 26-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                                 STRANDEDNESS:
                    TISSUE TYPE:
                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                            TELEX: 421792
                                                                                                                                                                                                                                                                                           TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
CELL TYPE:
                                                        DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                        NAME:
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                                                                         INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                             (212) 751-6849
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                                                                                                             mouse
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BASED ON ALLOIMMUNIZATION WITH ZONA PELLUCIDA
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FEATURE: NAME/KEY:

ZP2

ORGANELLE

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seq_documentation_block:
; Sequence 7, Applicatio
; Patent No. 5641487
; GENERAL INFORMATION:
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US-09-684-016-48411 x US-08-453-472-6
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    Quality:
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                                                                                            FILING DATE: 20-AUG-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/364,379

FILING DATE: 12-JUN-1989

ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 99152/E-26

TELECOMMUNICATION INFORMATION:
                   TELEPHONE: (202) 861-:
TELEFAX: (202) 822-094
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 alTyrSerHisGln 379
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 26-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S. ZIP: 20005-3918
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                                                                                 (202) 861-3000
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Gaps: 2
Percent Identity: 34.211
                                                                                                                    99152/E-266-88/2
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alignment_block:
US-09-684-016-48411 x US-08-038-948-7
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-038-948-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08038948 Patent No. 5641487
TELEPHONE: (202) 861-3
TELEPAX: (202) 822-094
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                          ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WALSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 9915
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: DEAN,
                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,462
FILING DATE: 20-AUG-1992
PRIOR APPLICATION NUMBER: US 07/364,379
FILING DATE: 12-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 TTTATTCCACACAA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 CysHisCysGluSerProValSerIleAspGluLeuCysAlaGln...As 368
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                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 26-MAR CLASSIFICATION: 435
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TYPE: a
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                                                            822-0944
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Gaps: 2
Percent Identity: 34.211
                                                                                                                    99152/E-266-88/2
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-038-948-8
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US-09-684-016-48411 x US-08-038-948-8
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                                                                                                 APPLICATION NUMBER: US 07/364,379
FILING DATE: 12-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 99152/E-266-88/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEPAX: (202) 822-0944
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                                      TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/930,462 FILING DATE: 20-AUG-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DEAN, JURRIEN
TITLE OF INVENTION: CONTRACEPTIVE VACCINE BASED ON
TITLE OF INVENTION: ALLOIMMUNIZATION WITH ZONA PELLUCIDA POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-MAR-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
                     LENGTH:
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20005-3918
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713 amino acids
nino acid
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SYSTEM: PC-DOS/MS-DOS
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34.211
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; STRANDEDNESS:
; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-038-948-10
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6,
                                                                  APPLICATION NUMBER: US 07/930,462
FILLING DATE: 20-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/364,379
FILLING DATE: 12-JUN-1989
ATTORNEY/ACENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4032 |
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DEAN, JUITITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 01 FILING DATE: 26-MAR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 alTyrSerHisGln 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 GGGCTGCACTGACTGGTAAGTTTCACATGTAAGGTGATACTTATCTTCAA 107
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STATE:
                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 30-May
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA 57
                                                      TELEPHONE:
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                                   (212) 758-4800
(212) 751-6849
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                                                                                                                                                                                                                                                                                                                                                             30-May-1995
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2.553
50.000
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                                                                                                                                                                                                                                                                                                    US 08/038,948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....GluV 375
                                                                                           2026-4032 US
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2
34.211
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SEQUENCE CHARACTERISTICS:

ENGTH:

amino acid

STRANDEDNESS: TOPOLOGY: unl

unknown

single

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seq_documentation_block:
; Sequence 6, Application US/08862903
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US-09-684-016-48411 x US-08-453-952-6
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                       TITLE OF INVENTION: IT TITLE OF INVENTION: IT TITLE OF INVENTION: IT TITLE OF SEQUENCES:
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 pGlyPheMetAspPhe....
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                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 TTTATTCCACACAA 121
                                                                                                                                                                                      STREET: 345 PA
CITY: NEW YORK
STATE: NEW YOR
CLASSIFICATION:
                              APPLICATION NUMBER: US/08/862,903
                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                        10154
                                                                                                                                                                                      NEW YORK
                                                                                                                                                                                                                       345 PARK AVENUE
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                 30-May-1995
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                                                                                                                                                                                                                                                                                                                           CONTRACEPTIVE VACCINE
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Gaps: 2
Percent Identity: 34.211
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; IDENTIFICATION METHOD: ; OTHER INFORMATION: mo US-08-862-903-6
                                                                                                        seq_documentation_block:
                                                                                                                                          seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-549-515-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                     Sequence 6, Application US/08549515 Patent No. 6054123
                  GENERAL INFORMATION:
APPLICANT: LOOSMO
APPLICANT: Klein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
APPLICANT: Loosmore, Sheena APPLICANT: Klein, Michel H TITLE OF INVENTION: Haemoph
                                                                                                                                                                                                               108 TTTATTCCACACAA 121
                                                                                                                                                                                                                                                    368 pGlyPheMetAspPhe......GluV 375
                                                                                                                                                                                                                                                                                                                         353 CysHisCysGluSerProValSerIleAspGluLeuCysAlaGln...As 368
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                                                                                                                                                                             375 alTyrSerHisGln 379
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                                                                                                                                                                                                                                                                                      58 GGGCTGCACTGACTGGTAAGTTTCACATGTAAGGTGATACTTATCTTCAA 107
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LOCATION:
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STRANDEDNESS: sir
TOPOLOGY: unknown
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TELEX: 421792
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212) 751-6849
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Percent Identity: 34.211
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Haemophilus Influenzae

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alignment_block: US-09-684-016-48411 x US-08-549-515-6
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                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08549515 Patent No. 6054123
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              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
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119 nLysGlyHisMetThrLysCysAspGlyCys 129
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                APPLICANT: LOOSMORE, Sheena M
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Haemophilu
TITLE OF INVENTION: Dimethyls
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 ArgTyrCysHisMetAlaCysProTyrAspAlaProGlnTyrAspAlaGl 119
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ATTORNEY/AGENT INFORMATION:
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COMPUTER:
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                                                                          COUNTRY:
                                                                                                                                 STREET:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                    ку: Canada
MSG 1R7
                                                                                                             Toronto
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                                                                                             Ontario
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                                                                                                                               Suite 701,
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Suite 701, 330 Unviersity Avenue
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                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC condible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                APPLICATION NUMBER: US/O:
FILING DATE: 25-MAY-1994
CLASSIFICATION: 514
ATTONNEY/AGENT INFORMATION:
NAME: Wallen, John W.
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wallen, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cully, Doris F.
APPLICANT: Arena, Joseph P.
APPLICANT: Liu, Ken K.
APPLICANT: Vassilatis, Demetrics
TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE
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LENGTH: 205 amino acids
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APPLICATION NUMBER: US/08/549,515
FILING DATE: 27-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DNA ENCOR
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REGISTRATION NUMBER: REFERENCE/DOCKET NUM
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Y: U.S.A.
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  NUMBER:
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n Release #1.0, Version #1.30
                                                                                                                                                     Release #1.0, Version #1.25
                                                                                                               US/08/249,112
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  19194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
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TELECOMMUNICATION INFORMATION:

(806)

594-3905

ELEPHONE:

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seq_name: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:PCT-US95-06556-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-249-112-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-684-016-48411/rev x US-08-249-112-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249
FILING DATE: 25 MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          equence 4, Application:
                                        TELEFAX: (908) 594-4720
NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     documentation_block:
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Liu, Ken K.
APPLICANT: Vassilatis, Demetrios
TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE
TITLE OF INVENTION: CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 gLeuGlnLeuTyrProLeuAspTyrGlnSerCys 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 LysIleLeuTyrSerSerArgIleSerLeuThrSerSerCysProMetAr 168
                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 CATTGCG.....CCATTAGGTCATCAGGGTTGT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/06556
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 07065
                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rahway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Wallen, John W.
126 E. Lincoln Ave., P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arena,
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67.857
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                                                         594-4720
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                                                                                                                                                                                                                            US 08/249,112
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                                                                                                                        19194
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alignment_block:
US-09-684-016-48411/rev x PCT-US95-06556-4
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-06556-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-211-704A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
                                                                               TELEFAX: (650)496-1200 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 09/
FILING DATE: 09-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,09
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                             REFERENCE/DOCKET NUMBER: SE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-3196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 gLeuGlnLeuTyrProLeuAspTyrGlnSerCys 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 CATTGCG.....CCATTAGGTCATCAGGGTTGT 27
               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7, Application US/09211704A
). 6271014
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                                                  amino acid
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                                                                 519 amino acids
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                                                                                                (650)496-1200
TN NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fossiez, Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       de Saint-Vis, Blandine
                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNAX Research Institute
peptide
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67.857
                               not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serge J.E.
                                                                                                                                                                                                                                                   us 09/005,263
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                                                                                                                                                                                 34,090
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                                                                                                                                                                  SF0781K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487
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alignment_scores:
Quality:
Ratio:
                                                                                                                               seq_documentation_block:
                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-357-598-12
                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-684-016-48411 x US-09-115-954-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 714
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-115-954-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jupe, Steven C
APPLICANT: Day, Christopher J
APPLICANT: Rawlings, Christopher J
APPLICANT: Doe, Trudy R
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409
CURRENT APPLICATION NUMBER: US/09/115,954B
CURRENT FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: EP97401714.7
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores
                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-09-115-954-4 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-684-016-48411/rev x US-09-211-704A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                        Sequence 12, Application US/08357598 Patent No. 5705625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 4, Application US/09115954B Patent No. 6200776
      GENERAL INFORMATION:
APPLICANT: Civin, (
APPLICANT: Small, I
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Martin, Xavier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Boron, Walter F
APPLICANT: Bril, Antoine M
APPLICANT: Khandoudi, Nassirah
                                                                                                                                                                                                                 305 TyrCysArgCysThrLeuProGluAsnProAsnAsn 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 TGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTACCAGTCA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 gThrPheProArgAspSerProLeuGlyHisAspThrValArgAlaLeuM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 GTGCAGCCCTCGCATTGCGCCATTAGGTCATCAGGGTTGTAAGGCATCTC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 TrpAsnLysArgAsnLeuSerTrpArgVal.....Ar
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                                                                                                                                                                                                                                       5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-115-954-4
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2.526
52.778
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4.800
83.333
Donald
:: NOVEL PROTEIN TYROSINE KINASE, JAK3
                                                 Curt I.
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Percent Identity:
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Percent Identity:
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-357-598-12
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                                                                                                                                                                                                                                       seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-357-598-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                  Sequence 12, Application US/09003289 Patent No. 5916792
                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: 619/678-509
INFORMATION FOR SEC. 75.
                                                                                               APPLICANT: Civin, Curt I.
APPLICANT: Small, Donald
TITLE OF INVENTION: NOVEL I
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/357,598
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORWATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                           340 euSerHis 342
                                                                                                                                                                                                                                                                                                                                                                          323 uGlyProAspTyrLysGlyCysLeuIleArgProGlyPheLeuValGlyL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                            312 AspAspSerPheLeuLeuThrCys......ValGlnProLe 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          20 TCTCACAT 13
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                                     STATE:
                                                     CITY:
                                                                   STREET:
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                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-09-003-289-12
E: CA
TRY: USA
92037
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                                                   La Jolla
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                                                                   4225 Executive Square, Suite 1400
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                    Fish & Richardson P.C
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                                                                                                                                      NOVEL PROTEIN TYROSINE KINASE,
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38.889
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alignment_block:
US-09-684-016-48411/rev x US-09-003-289-12
                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                 equence 12, Application PC/TUS9516435
               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                    STREET: **-
STREET: TO JOLIA
CITY: LA JOLIA
CTATE: CA
                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619,678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 15-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 846 amino acid
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                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                             APPLICANT: The Johns Hopkins University School of medicine TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 euSerHis 342
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
  APPLICATION NUMBER:
                                                                                                                                                              COUNTRY:
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/003,289
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15-DEC-1994
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2.400
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PCT/US95/16435
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-115-954-8
                                                          alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-115-954-8
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   Ratio:
Percent Similarity:
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                                                                                                                                                                                        SEQ ID NO 8
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                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: EP97401714.7
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/115,954B CURRENT FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                     APPLICANT: Jupe, Steven C
APPLICANT: Rawlings, Christopher J
APPLICANT: Doe, Trudy R
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Boron, Walter F APPLICANT: Bril, Antoine M
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NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                            SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Martin, Xavier
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Khandoudi, Nassirah
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                                                                                                                                                                       LENGTH:
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CLASSIFICATION:
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                                      Quality:
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Length: 12
Gaps: 0
Percent Identity: 50.000
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Gaps:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 1044
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-115-954-2
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US-09-684-016-48411 x US-09-115-954-8
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                                                             NUMBER OF SEQ ID NOS: 29
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/09352990 Patent No. 6255090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2
                                                                                                                                                            APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
FILE REFERENCE: BB-1191
CURRENT APPLICATION NUMBER: US/09/352,990
CURRENT FILING DATE: 1999-07-14
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                                                                                                                       EARLIER APPLICATION NUMBER: 60/092,866
EARLIER FILING DATE: July 15, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/115,954B CURRENT FILING DATE: 1998-07-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL COMPOUNDS FILE REFERENCE: GH-30409
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ORGANISM: Glycine max
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                                            ENGTH:
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5. 6200776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rawlings, Christopher J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jupe, Steven C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Khandoudi, Nassirah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: US-09-115-954-2 from: 1
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4.800
83.333
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; MOLECULE TYPE: US-08-445-586-9
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US-09-684-016-48411/rev x US-09-352-990-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                              TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NATA:
PRIOR APPLICATION NUMBER: US 08/111,887
APPLICATION NUMBER: J6-AUG-1993
APPLICATION NUMBER: JP 330030/92
FILING DATE: 28-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005-3314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                               REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                             FILING DATE: 03-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Bone-Related Sulfatase-Like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 gLeuAlaPro 23
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                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                     LENGTH:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9, Application US/08445586
5, 5627050
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                                                      amino acid
                                                                                                                                                                                                                         Forman, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.C.
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                                                                       583 amino acids
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1300 I Street, N.W.
                                                                                                                                202-408-4400
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                                                                                                                                                   202-408-4000
                   peptide
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03~DEC-1992
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3.133
75.000
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                                                                                                              9:
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                                                                                                                                                                                      02481.1322-00000
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to:
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US-08-484-493-14
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US-09-684-016-48411/rev x US-08-445-586-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-484-493-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/08484493 Patent No. 5728381
                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: D1619110, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 84162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                  TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,493
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF TITLE OF INVENTION: IDURONATE 2-SULFATASE NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           486 1 486
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                                                  STRANDEDNESS:
                                    TOPOLOGY:
                                                                                                                                                                       TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                         amino acid
                                                                                           583 amino acids
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Clements, Peter R
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                                    linear
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3.357
82.353
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Donald S
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Gaps: 0
Percent Identity: 41.176
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-484-494-14
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; Sequence 14, Applicati
; Patent No. 5798239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-484-494-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 991,973
APPLICATION NUMBER: 991,973
FILING DATE: 17-DCC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO: Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-343
                                                                                                                         TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/484,494
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                             TELEPHONE: 510-742-4366
                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Garden City
STATE: New York
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                                                                                     LENGTH:
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                                                                    amino acid
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Anson, Donald S
Occhican
                                                                                   583 amino acids
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Clements, Peter R
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                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
                                     linear
                protein
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3.357
82.353
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Gaps: 0
Percent Identity: 41.176
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alignment\_scores:
 Quality:

47.00

Length:

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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-345-212-14
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US-09-684-016-48411/rev x US-08-484-494-14
                                                                           alignment_scores:
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                             Ratio:
Percent Similarity:
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Percent Similarity:
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                                                                                                                                                                                                                  TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
                                                                                                                                                                                                                                                                                                              FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: D161glio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416Z
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,9
FILING DATE: 17-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 400 CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: 516-742-4343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                  CENGTH:
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                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11530
                                                                                                                                                                                  H: 583 amino acids amino acid
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5932211
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                                                                                                                                                                                                                                                                     516-742-4366
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17
Gaps: 0
Percent Identity: 41.176
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Percent Identity: 41.176
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alignment_block:
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; MOLECULE TYPE:
US-09-249-003-14
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US-09-684-016-48411/rev x US-08-345-212-14
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                                     Percent Similarity:
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                                                                                                                                                                                                                                                              TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/991
PRILING DATE: 17-DEC-1992
PRILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S
REGISTRATION NUMBER: 31,34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acid
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                                                                                                                                                                                                            TYPE:
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REFERENCE/DOCKET NUMBER: 8416Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                     Quality:
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F: 400 Garden City Plaza
Garden City
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Clements, Peter R
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Anson, Donald S
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                              Gaps: 0
Percent Identity: 41.176
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Align seg 1/1 to: US-09-249-003-14

from: 1

to: 583

US-09-684-016-48411/rev x US-09-249-003-14

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; NAME/KEY: CDS
; LOCATION: 1831..4290
; OTHER INFORMATION: /n
US-08-374-483-2
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Quality:
Ratio:
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                                                                                 Align seg 1/1 to: US-08-374-483-2
                                                                                                                     US-09-684-016-48411 x US-08-374-483-2
                                                                                                                                                                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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372 CysSerGlnProTyrProSerGlyAspSerCysCysAlaGluProProAl 388
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NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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APPLICANT: BLAZING, MICHAEL A.
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                                     14 TGTGAGATGCCTTACAACCCTGATGACCTAATG.......
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 816-4100 TELEX: 200797 NIXN UR
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CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 820 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                           Percent Identity: 40.000
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alignment_block: US-09-684-016-48411 x US-08-374-483-5
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US-08-374-483-5
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                                                                                                                                         Align seg 1/1 to: US-08-374-483-5 from: 1
                                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                       372 CysSerGlnProTyrProSerGlyAspSerCysCysAlaGluProProAl 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GEORGE, SAMUEL E.
APPLICANT: BLAZING, MICHAEL A.
TITLE OF INVENTION: ADENOVIRAL VECTOR SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                  49 GCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGTA 88
                                                                                                      49 GCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGTA 88
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CITY: ARLINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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Quality:
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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SYSTEM: PC-DOS/MS-DOS
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Percent Identity:
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